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Jacqueline Elizabeth Shea

<120> Attenuated Salmonella SPI2 Mutants as Antigen Carriers

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<150> PCT/EP99/06514

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aaagctacat atcagtataa aaaccgtcga aacacaccgg atgaatatga tgagaaagct 3600
acaggttcat aaagtacag agttacttaa ctgtgccga agaatgaggt taatagagta 3660
ttaaccaggg gcgtccgatg gtattaagca ttggtcatat tttgatgagc cttacgccac 3720
gcagtattgc tcatcatcga caaaatccat acggatgccg tggatgccg caccatttat 3780
cactacctta gtcttcattt gatcatgata tagtagaatc cccttattta acgggcttta 3840
ccatgtcgta ttctatcggc gaatttgcca gactatgcgg tatcaatgcc gccacgctaa 3900
gggcatggca gcgacgctat g                                     3921

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<210> 3  
 <211> 327  
 <212> DNA  
 <213> Salmonella

<220>  
 <221> CDS  
 <222> (1) .. (324)

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Met Met Ile Lys Lys Lys Ala Ala Phe Ser Glu Tyr Arg Asp Leu Glu
  1                      5                      10                      15

caa agt tac atg cag cta aat cac tgt ctt aaa aaa ttt cac caa atc 96
Gln Ser Tyr Met Gln Leu Asn His Cys Leu Lys Lys Phe His Gln Ile
                20                25                30

cgg gct aag gtg agt caa cag ctt gct gaa agg gca gag agc ccc aaa 144
Arg Ala Lys Val Ser Gln Gln Leu Ala Glu Arg Ala Glu Ser Pro Lys
        35                40                45

aat agc aga gag aca gag agt att ctt cat aac cta ttt cca caa ggc 192
Asn Ser Arg Glu Thr Glu Ser Ile Leu His Asn Leu Phe Pro Gln Gly
        50                55                60

gtt gcc ggg gtt aac cag gag gcc gag aag gat tta aag aaa ata gta 240
Val Ala Gly Val Asn Gln Glu Ala Glu Lys Asp Leu Lys Lys Ile Val
        65                70                75                80

agt ttg ttt aaa caa ctt gaa gta cga ctg aaa caa ctt aat gct caa 288
Ser Leu Phe Lys Gln Leu Glu Val Arg Leu Lys Gln Leu Asn Ala Gln
                85                90                95

gcc ccg gtg gag ata ccg tca gga aaa aca aaa agg taa 327
Ala Pro Val Glu Ile Pro Ser Gly Lys Thr Lys Arg

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100

105

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 <212> PRT  
 <213> Salmonella

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 Gln Ser Tyr Met Gln Leu Asn His Cys Leu Lys Lys Phe His Gln Ile  
                   20                  25                  30  
 Arg Ala Lys Val Ser Gln Gln Leu Ala Glu Arg Ala Glu Ser Pro Lys  
           35                  40                  45  
 Asn Ser Arg Glu Thr Glu Ser Ile Leu His Asn Leu Phe Pro Gln Gly  
           50                  55                  60  
 Val Ala Gly Val Asn Gln Glu Ala Glu Lys Asp Leu Lys Lys Ile Val  
           65                  70                  75                  80  
 Ser Leu Phe Lys Gln Leu Glu Val Arg Leu Lys Gln Leu Asn Ala Gln  
                   85                  90                  95  
 Ala Pro Val Glu Ile Pro Ser Gly Lys Thr Lys Arg  
           100                  105

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           1                  5                  10                  15  
 aaa aat agc ttc ggc gtc agc aac gct gat acc ggg agc cag gat gac 96  
 Lys Asn Ser Phe Gly Val Ser Asn Ala Asp Thr Gly Ser Gln Asp Asp  
                   20                  25                  30  
 tta tcc cag caa aat ccg ttt gcc gaa ggg tat ggt gtt ttg ctt att 144  
 Leu Ser Gln Gln Asn Pro Phe Ala Glu Gly Tyr Gly Val Leu Leu Ile  
           35                  40                  45  
 ctc ctt atg gtt att cag gct atc gca aat aat aaa ttt att gaa gtc 192  
 Leu Leu Met Val Ile Gln Ala Ile Ala Asn Asn Lys Phe Ile Glu Val  
           50                  55                  60

cag aag aac gct gaa cgt gcc aga aat acc cag gaa aag tca aat gag	240
Gln Lys Asn Ala Glu Arg Ala Arg Asn Thr Gln Glu Lys Ser Asn Glu	
65 70 75 80	

atg gat gag gtg att gct aaa gca gcc aaa ggg gat gct aaa acc aaa	288
Met Asp Glu Val Ile Ala Lys Ala Ala Lys Gly Asp Ala Lys Thr Lys	
85 90 95	

gag gag gtg cct gag gat gta att aaa tac atg cgt gat aat ggt att	336
Glu Glu Val Pro Glu Asp Val Ile Lys Tyr Met Arg Asp Asn Gly Ile	
100 105 110	

ctc atc gat ggt atg acc att gat gat tat atg gct aaa tat ggc gat	384
Leu Ile Asp Gly Met Thr Ile Asp Asp Tyr Met Ala Lys Tyr Gly Asp	
115 120 125	

cat ggg aag ctg gat aaa ggt ggc cta cag gcg atc aaa gcg gct ttg	432
His Gly Lys Leu Asp Lys Gly Gly Leu Gln Ala Ile Lys Ala Ala Leu	
130 135 140	

gat aat gac gcc aac cgg aat acc gat ctt atg agt cag ggg cag ata	480
Asp Asn Asp Ala Asn Arg Asn Thr Asp Leu Met Ser Gln Gly Gln Ile	
145 150 155 160	

aca att caa aaa atg tct cag gag ctt aac gct gtc ctt acc caa ctg	528
Thr Ile Gln Lys Met Ser Gln Glu Leu Asn Ala Val Leu Thr Gln Leu	
165 170 175	

aca ggg ctt atc agt aag tgg ggg gaa att tcc agt atg ata gcg cag	576
Thr Gly Leu Ile Ser Lys Trp Gly Glu Ile Ser Ser Met Ile Ala Gln	
180 185 190	

aaa acg tac tca tga	591
Lys Thr Tyr Ser	
195	

<210> 6  
 <211> 196  
 <212> PRT  
 <213> Salmonella

<400> 6	
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Lys Asn Ser Phe Gly Val Ser Asn Ala Asp Thr Gly Ser Gln Asp Asp	
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Leu Ser Gln Gln Asn Pro Phe Ala Glu Gly Tyr Gly Val Leu Leu Ile	
35 40 45	

Leu Leu Met Val Ile Gln Ala Ile Ala Asn Asn Lys Phe Ile Glu Val	
50 55 60	

Gln Lys Asn Ala Glu Arg Ala Arg Asn Thr Gln Glu Lys Ser Asn Glu	
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tca ttg cct gac ttt ttg cag acc aat ccc gcg gtt tta tca atg atg	288
Ser Leu Pro Asp Phe Leu Gln Thr Asn Pro Ala Val Leu Ser Met Met	
85 90 95	
atg acg tca tta ata ctc aac gtc ttt ggt aat aac gct caa tcg tta	336
Met Thr Ser Leu Ile Leu Asn Val Phe Gly Asn Asn Ala Gln Ser Leu	
100 105 110	
tgc caa cag ctt gag cgg gca act gag gtg caa aat gca tta cgt aat	384
Cys Gln Gln Leu Glu Arg Ala Thr Glu Val Gln Asn Ala Leu Arg Asn	
115 120 125	
aag cag gta aag gag tat cag gag cag atc cag aaa gcg ata gag cag	432
Lys Gln Val Lys Glu Tyr Gln Glu Gln Ile Gln Lys Ala Ile Glu Gln	
130 135 140	
gag gat aaa gcg cgt aaa gcg ggt att ttt ggc gct att ttt gac tgg	480
Glu Asp Lys Ala Arg Lys Ala Gly Ile Phe Gly Ala Ile Phe Asp Trp	
145 150 155 160	
att acc ggc ata ttt gaa acc gtg att ggc gcc tta aaa gtt gtg gaa	528
Ile Thr Gly Ile Phe Glu Thr Val Ile Gly Ala Leu Lys Val Val Glu	
165 170 175	
ggt ttt ctg tcc gga aat ccc gca gaa atg gct agc ggc gta gct tat	576
Gly Phe Leu Ser Gly Asn Pro Ala Glu Met Ala Ser Gly Val Ala Tyr	
180 185 190	
atg gcc gca ggt tgt gca gga atg gtt aaa gcc gga gcc gaa acg gca	624
Met Ala Ala Gly Cys Ala Gly Met Val Lys Ala Gly Ala Glu Thr Ala	
195 200 205	
atg atg tgc ggt gct gac cac gat acc tgt cag gca att att gac gtg	672
Met Met Cys Gly Ala Asp His Asp Thr Cys Gln Ala Ile Ile Asp Val	
210 215 220	
aca agt aag att caa ttt ggt tgt gaa gcc gtc gcg ctg gca ctg gat	720
Thr Ser Lys Ile Gln Phe Gly Cys Glu Ala Val Ala Leu Ala Leu Asp	
225 230 235 240	
gtt ttc cag att ggc cgt gct ttt atg gcg acg aga ggt tta tct ggc	768
Val Phe Gln Ile Gly Arg Ala Phe Met Ala Thr Arg Gly Leu Ser Gly	
245 250 255	
gca gct gca aaa gtg ctt gac tcc ggt ttt ggc gag gaa gtg gtt gag	816
Ala Ala Ala Lys Val Leu Asp Ser Gly Phe Gly Glu Glu Val Val Glu	
260 265 270	
cgt atg gta ggt gca ggg gaa gca gaa ata gag gag ttg gct gaa aag	864
Arg Met Val Gly Ala Gly Glu Ala Glu Ile Glu Glu Leu Ala Glu Lys	
275 280 285	
ttt ggc gaa gaa gtg agc gaa agt ttt tcc aaa caa ttt gag ccg ctt	912
Phe Gly Glu Glu Val Ser Glu Ser Phe Ser Lys Gln Phe Glu Pro Leu	
290 295 300	

gaa cgt gaa atg gct atg gcg aat gag atg gca gag gag gct gcc gag	960
Glu Arg Glu Met Ala Met Ala Asn Glu Met Ala Glu Glu Ala Ala Glu	
305 310 315 320	
ttt tct cgt aac gta gaa aat aat atg acg cga agc gcg gga aaa agc	1008
Phe Ser Arg Asn Val Glu Asn Asn Met Thr Arg Ser Ala Gly Lys Ser	
325 330 335	
ttt acg aaa gag ggg gtg aaa gcc atg gca aaa gaa gcg gca aaa gaa	1056
Phe Thr Lys Glu Gly Val Lys Ala Met Ala Lys Glu Ala Ala Lys Glu	
340 345 350	
gcc ctg gaa aaa tgt gtg caa gaa ggt gga aag ttc ctg tta aaa aaa	1104
Ala Leu Glu Lys Cys Val Gln Glu Gly Gly Lys Phe Leu Leu Lys Lys	
355 360 365	
ttc cgt aat aaa gtt ctc ttc aat atg ttc aaa aaa atc ctg tat gcc	1152
Phe Arg Asn Lys Val Leu Phe Asn Met Phe Lys Lys Ile Leu Tyr Ala	
370 375 380	
tta ctg agg gat tgt tca ttt aaa ggc tta cag gct atc aga tgt gca	1200
Leu Leu Arg Asp Cys Ser Phe Lys Gly Leu Gln Ala Ile Arg Cys Ala	
385 390 395 400	
acc gag ggc gcc agt cag atg aat act ggc atg gtt aac aca gaa aaa	1248
Thr Glu Gly Ala Ser Gln Met Asn Thr Gly Met Val Asn Thr Glu Lys	
405 410 415	
gcg aag atc gaa aag aaa ata gag caa tta ata act cag caa cgg ttt	1296
Ala Lys Ile Glu Lys Lys Ile Glu Gln Leu Ile Thr Gln Gln Arg Phe	
420 425 430	
ctg gat ttc ata atg caa caa aca gaa aac cag aaa aag ata gaa caa	1344
Leu Asp Phe Ile Met Gln Gln Thr Glu Asn Gln Lys Lys Ile Glu Gln	
435 440 445	
aaa cgc tta gag gag ctt tat aag ggg acg ggt gcc gcg ctt aga gat	1392
Lys Arg Leu Glu Glu Leu Tyr Lys Gly Thr Gly Ala Ala Leu Arg Asp	
450 455 460	
gta tta gat acc att gat cac tat agt agc gtt cag gcg aga ata gct	1440
Val Leu Asp Thr Ile Asp His Tyr Ser Ser Val Gln Ala Arg Ile Ala	
465 470 475 480	
ggc tat cgc gct taa	1455
Gly Tyr Arg Ala	

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<211> 484

<212> PRT

<213> Salmonella

<400> 8

Met Asn Arg Ile His Ser Asn Ser Asp Ser Ala Ala Gly Val Thr Ala
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Leu	Thr	His	His	His	Leu	Ser	Asn	Val	Ser	Cys	Val	Ser	Ser	Gly	Ser		
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Leu	Gly	Lys	Arg	Gln	His	Arg	Val	Asn	Ser	Thr	Phe	Gly	Asp	Gly	Asn		
		35					40					45					
Ala	Ala	Cys	Leu	Leu	Ser	Gly	Lys	Ile	Ser	Leu	Gln	Glu	Ala	Ser	Asn		
	50					55					60						
Ala	Leu	Lys	Gln	Leu	Leu	Asp	Ala	Val	Pro	Gly	Asn	His	Lys	Arg	Pro		
65					70					75					80		
Ser	Leu	Pro	Asp	Phe	Leu	Gln	Thr	Asn	Pro	Ala	Val	Leu	Ser	Met	Met		
				85					90					95			
Met	Thr	Ser	Leu	Ile	Leu	Asn	Val	Phe	Gly	Asn	Asn	Ala	Gln	Ser	Leu		
			100					105					110				
Cys	Gln	Gln	Leu	Glu	Arg	Ala	Thr	Glu	Val	Gln	Asn	Ala	Leu	Arg	Asn		
		115					120					125					
Lys	Gln	Val	Lys	Glu	Tyr	Gln	Glu	Gln	Ile	Gln	Lys	Ala	Ile	Glu	Gln		
	130					135					140						
Glu	Asp	Lys	Ala	Arg	Lys	Ala	Gly	Ile	Phe	Gly	Ala	Ile	Phe	Asp	Trp		
145					150					155					160		
Ile	Thr	Gly	Ile	Phe	Glu	Thr	Val	Ile	Gly	Ala	Leu	Lys	Val	Val	Glu		
				165					170					175			
Gly	Phe	Leu	Ser	Gly	Asn	Pro	Ala	Glu	Met	Ala	Ser	Gly	Val	Ala	Tyr		
		180						185					190				
Met	Ala	Ala	Gly	Cys	Ala	Gly	Met	Val	Lys	Ala	Gly	Ala	Glu	Thr	Ala		
	195						200					205					
Met	Met	Cys	Gly	Ala	Asp	His	Asp	Thr	Cys	Gln	Ala	Ile	Ile	Asp	Val		
	210					215					220						
Thr	Ser	Lys	Ile	Gln	Phe	Gly	Cys	Glu	Ala	Val	Ala	Leu	Ala	Leu	Asp		
225					230					235					240		
Val	Phe	Gln	Ile	Gly	Arg	Ala	Phe	Met	Ala	Thr	Arg	Gly	Leu	Ser	Gly		
				245					250					255			
Ala	Ala	Ala	Lys	Val	Leu	Asp	Ser	Gly	Phe	Gly	Glu	Glu	Val	Val	Glu		
			260					265					270				
Arg	Met	Val	Gly	Ala	Gly	Glu	Ala	Glu	Ile	Glu	Glu	Leu	Ala	Glu	Lys		
		275					280					285					
Phe	Gly	Glu	Glu	Val	Ser	Glu	Ser	Phe	Ser	Lys	Gln	Phe	Glu	Pro	Leu		
	290					295					300						
Glu	Arg	Glu	Met	Ala	Met	Ala	Asn	Glu	Met	Ala	Glu	Glu	Ala	Ala	Glu		
305					310					315					320		

Phe Ser Arg Asn Val Glu Asn Asn Met Thr Arg Ser Ala Gly Lys Ser  
                   325                  330                  335  
 Phe Thr Lys Glu Gly Val Lys Ala Met Ala Lys Glu Ala Ala Lys Glu  
                   340                  345                  350  
 Ala Leu Glu Lys Cys Val Gln Glu Gly Gly Lys Phe Leu Leu Lys Lys  
                   355                  360                  365  
 Phe Arg Asn Lys Val Leu Phe Asn Met Phe Lys Lys Ile Leu Tyr Ala  
                   370                  375                  380  
 Leu Leu Arg Asp Cys Ser Phe Lys Gly Leu Gln Ala Ile Arg Cys Ala  
 385                  390                  395                  400  
 Thr Glu Gly Ala Ser Gln Met Asn Thr Gly Met Val Asn Thr Glu Lys  
                   405                  410                  415  
 Ala Lys Ile Glu Lys Lys Ile Glu Gln Leu Ile Thr Gln Gln Arg Phe  
                   420                  425                  430  
 Leu Asp Phe Ile Met Gln Gln Thr Glu Asn Gln Lys Lys Ile Glu Gln  
                   435                  440                  445  
 Lys Arg Leu Glu Glu Leu Tyr Lys Gly Thr Gly Ala Ala Leu Arg Asp  
                   450                  455                  460  
 Val Leu Asp Thr Ile Asp His Tyr Ser Ser Val Gln Ala Arg Ile Ala  
 465                  470                  475                  480  
 Gly Tyr Arg Ala

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 <211> 504  
 <212> DNA  
 <213> Salmonella

<220>  
 <221> CDS  
 <222> (1)..(501)

<400> 9  
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   1                  5                  10                  15  
 cta atg gag ctt gcc aaa aag ctg cgc gat atc atg cgc agc tat aac 96  
 Leu Met Glu Leu Ala Lys Lys Leu Arg Asp Ile Met Arg Ser Tyr Asn  
                   20                  25                  30  
 gta gaa aaa caa cgg ctg gcc tgg gaa ctg caa gtc aat gtt tta cag 144  
 Val Glu Lys Gln Arg Leu Ala Trp Glu Leu Gln Val Asn Val Leu Gln  
                   35                  40                  45

acg	caa	atg	aaa	aca	att	gat	gaa	gcg	ttt	aga	gca	tca	atg	att	act	192
Thr	Gln	Met	Lys	Thr	Ile	Asp	Glu	Ala	Phe	Arg	Ala	Ser	Met	Ile	Thr	
	50					55					60					
gcg	ggt	ggc	gca	atg	ttg	tcg	ggt	gta	ctg	acg	ata	gga	tta	ggg	gcc	240
Ala	Gly	Gly	Ala	Met	Leu	Ser	Gly	Val	Leu	Thr	Ile	Gly	Leu	Gly	Ala	
65					70					75					80	
gta	ggc	ggg	gaa	acc	ggt	ctt	ata	gcg	ggt	caa	gcc	gta	ggc	cac	aca	288
Val	Gly	Gly	Glu	Thr	Gly	Leu	Ile	Ala	Gly	Gln	Ala	Val	Gly	His	Thr	
				85					90					95		
gct	ggg	ggc	gtc	atg	ggc	ctg	ggg	gct	ggt	gta	gcg	caa	cgt	caa	agt	336
Ala	Gly	Gly	Val	Met	Gly	Leu	Gly	Ala	Gly	Val	Ala	Gln	Arg	Gln	Ser	
			100					105					110			
gat	caa	gat	aaa	gcg	att	gcc	gac	ctg	caa	caa	aat	ggg	gcc	caa	tct	384
Asp	Gln	Asp	Lys	Ala	Ile	Ala	Asp	Leu	Gln	Gln	Asn	Gly	Ala	Gln	Ser	
			115					120					125			
tat	aat	aaa	tcc	ctg	acg	gaa	att	atg	gag	aaa	gca	act	gaa	att	atg	432
Tyr	Asn	Lys	Ser	Leu	Thr	Glu	Ile	Met	Glu	Lys	Ala	Thr	Glu	Ile	Met	
			130					135				140				
cag	caa	atc	atc	ggc	gtg	ggg	tcg	tca	ctg	gtc	acg	gtt	ctt	gct	gaa	480
Gln	Gln	Ile	Ile	Gly	Val	Gly	Ser	Ser	Leu	Val	Thr	Val	Leu	Ala	Glu	
145					150					155					160	
ata	ctc	cgg	gca	tta	acg	agg	taa									504
Ile	Leu	Arg	Ala	Leu	Thr	Arg										
				165												

<210> 10  
 <211> 167  
 <212> PRT  
 <213> Salmonella

<400> 10																
Met	Gly	Thr	Glu	Ser	Met	Leu	Leu	Leu	Phe	Asp	Asp	Ile	Trp	Met	Lys	
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Leu	Met	Glu	Leu	Ala	Lys	Lys	Leu	Arg	Asp	Ile	Met	Arg	Ser	Tyr	Asn	
			20					25					30			
Val	Glu	Lys	Gln	Arg	Leu	Ala	Trp	Glu	Leu	Gln	Val	Asn	Val	Leu	Gln	
		35					40					45				
Thr	Gln	Met	Lys	Thr	Ile	Asp	Glu	Ala	Phe	Arg	Ala	Ser	Met	Ile	Thr	
		50				55					60					
Ala	Gly	Gly	Ala	Met	Leu	Ser	Gly	Val	Leu	Thr	Ile	Gly	Leu	Gly	Ala	
65					70					75					80	
Val	Gly	Gly	Glu	Thr	Gly	Leu	Ile	Ala	Gly	Gln	Ala	Val	Gly	His	Thr	
				85					90					95		

Ala Gly Gly Val Met Gly Leu Gly Ala Gly Val Ala Gln Arg Gln Ser  
100 105 110

Asp Gln Asp Lys Ala Ile Ala Asp Leu Gln Gln Asn Gly Ala Gln Ser  
115 120 125

Tyr Asn Lys Ser Leu Thr Glu Ile Met Glu Lys Ala Thr Glu Ile Met  
130 135 140

Gln Gln Ile Ile Gly Val Gly Ser Ser Leu Val Thr Val Leu Ala Glu  
145 150 155 160

Ile Leu Arg Ala Leu Thr Arg  
165

<210> 11  
<211> 195  
<212> PRT  
<213> Salmonella

<400> 11  
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Thr Pro Ser Ser Thr Pro Ser Pro Ser Gly Glu Gly Met Gly Thr Glu  
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Ser Met Leu Leu Leu Phe Asp Asp Ile Trp Met Lys Leu Met Glu Leu  
35 40 45

Ala Lys Lys Leu Arg Asp Ile Met Arg Ser Tyr Asn Val Glu Lys Gln  
50 55 60

Arg Leu Ala Trp Glu Leu Gln Val Asn Val Leu Gln Thr Gln Met Lys  
65 70 75 80

Thr Ile Asp Glu Ala Phe Arg Ala Ser Met Ile Thr Ala Gly Gly Ala  
85 90 95

Met Leu Ser Gly Val Leu Thr Ile Gly Leu Gly Ala Val Gly Gly Glu  
100 105 110

Thr Gly Leu Ile Ala Gly Gln Ala Val Gly His Thr Ala Gly Gly Val  
115 120 125

Met Gly Leu Gly Ala Gly Val Ala Gln Arg Gln Ser Asp Gln Asp Lys  
130 135 140

Ala Ile Ala Asp Leu Gln Gln Asn Gly Ala Gln Ser Tyr Asn Lys Ser  
145 150 155 160

Leu Thr Glu Ile Met Glu Lys Ala Thr Glu Ile Met Gln Gln Ile Ile  
165 170 175

Gly Val Gly Ser Ser Leu Val Thr Val Leu Ala Glu Ile Leu Arg Ala

180

185

190

Leu Thr Arg  
195

<210> 12  
<211> 417  
<212> DNA  
<213> Salmonella

<220>  
<221> CDS  
<222> (1)..(414)

<400> 12  
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1 5 10 15  
  
gag cct gca tat tta ggg gag acc gcc ata tta ctt ggg cag cag ttt 96  
Glu Pro Ala Tyr Leu Gly Glu Thr Ala Ile Leu Leu Gly Gln Gln Phe  
20 25 30  
  
ata tta tcg cct tac ctg gtg atc tat cgt att gag gca aaa gaa atg 144  
Ile Leu Ser Pro Tyr Leu Val Ile Tyr Arg Ile Glu Ala Lys Glu Met  
35 40 45  
  
att att tgt gag ttc agg cgc ctg acg ccc ggg caa cct cga cca cag 192  
Ile Ile Cys Glu Phe Arg Arg Leu Thr Pro Gly Gln Pro Arg Pro Gln  
50 55 60  
  
caa ttg ttt cac tta ctg gga ctt tta cgc ggg ata ttt gtg cat cac 240  
Gln Leu Phe His Leu Leu Gly Leu Leu Arg Gly Ile Phe Val His His  
65 70 75 80  
  
ccg cag tta aca tgt tta aag atg ttg ata atc acc gac gtt ctg gat 288  
Pro Gln Leu Thr Cys Leu Lys Met Leu Ile Ile Thr Asp Val Leu Asp  
85 90 95  
  
gaa aaa aaa gcc atg cta cgc agg aaa tta ttg cgc atc ctg aca gta 336  
Glu Lys Lys Ala Met Leu Arg Arg Lys Leu Leu Arg Ile Leu Thr Val  
100 105 110  
  
atg gga gcg acc ttt aca cag ctt gat ggc gat aac tgg aca gtt tta 384  
Met Gly Ala Thr Phe Thr Gln Leu Asp Gly Asp Asn Trp Thr Val Leu  
115 120 125  
  
tcc gcc gag cat ctt atc cag cga cgt ttt taa 417  
Ser Ala Glu His Leu Ile Gln Arg Arg Phe  
130 135

<210> 13  
<211> 138  
<212> PRT

<213> Salmonella

<400> 13

Met	Val	Gln	Glu	Ile	Glu	Gln	Trp	Leu	Arg	Arg	His	Gln	Val	Phe	Thr	
1				5				10						15		
Glu	Pro	Ala	Tyr	Leu	Gly	Glu	Thr	Ala	Ile	Leu	Leu	Gly	Gln	Gln	Phe	
			20					25					30			
Ile	Leu	Ser	Pro	Tyr	Leu	Val	Ile	Tyr	Arg	Ile	Glu	Ala	Lys	Glu	Met	
		35					40					45				
Ile	Ile	Cys	Glu	Phe	Arg	Arg	Leu	Thr	Pro	Gly	Gln	Pro	Arg	Pro	Gln	
	50					55					60					
Gln	Leu	Phe	His	Leu	Leu	Gly	Leu	Leu	Arg	Gly	Ile	Phe	Val	His	His	
65				70						75					80	
Pro	Gln	Leu	Thr	Cys	Leu	Lys	Met	Leu	Ile	Ile	Thr	Asp	Val	Leu	Asp	
				85					90					95		
Glu	Lys	Lys	Ala	Met	Leu	Arg	Arg	Lys	Leu	Leu	Arg	Ile	Leu	Thr	Val	
			100					105					110			
Met	Gly	Ala	Thr	Phe	Thr	Gln	Leu	Asp	Gly	Asp	Asn	Trp	Thr	Val	Leu	
		115					120					125				
Ser	Ala	Glu	His	Leu	Ile	Gln	Arg	Arg	Phe							
	130					135										

<210> 14

<211> 789

<212> DNA

<213> Salmonella

<220>

<221> CDS

<222> (1) .. (786)

<400> 14

atg	aaa	att	cat	att	ccg	tca	gcg	gca	agt	aat	ata	gtc	gat	ggt	aat	48
Met	Lys	Ile	His	Ile	Pro	Ser	Ala	Ala	Ser	Asn	Ile	Val	Asp	Gly	Asn	
1				5				10						15		
agt	cct	cct	tcc	gat	ata	caa	gcg	aag	gag	gta	tcg	ttt	cct	ccc	cct	96
Ser	Pro	Pro	Ser	Asp	Ile	Gln	Ala	Lys	Glu	Val	Ser	Phe	Pro	Pro	Pro	
			20					25				30				
gaa	att	cca	gcg	cct	ggc	acc	ccc	gca	gcc	cct	gtg	ctg	ctt	acg	cct	144
Glu	Ile	Pro	Ala	Pro	Gly	Thr	Pro	Ala	Ala	Pro	Val	Leu	Leu	Thr	Pro	
		35					40					45				
gaa	caa	ata	agg	cag	cag	agg	gat	tat	gcg	ata	cat	ttt	atg	caa	tac	192
Glu	Gln	Ile	Arg	Gln	Gln	Arg	Asp	Tyr	Ala	Ile	His	Phe	Met	Gln	Tyr	
	50					55					60					



act att cgt gcg ctg ggt gcg aca gtc gtg ttt ggg tta tcg gtt gct	240
Thr Ile Arg Ala Leu Gly Ala Thr Val Val Phe Gly Leu Ser Val Ala	
65 70 75 80	
gca gcg gta att tct ggc ggg gca gga tta ccc att gct att ctt gcg	288
Ala Ala Val Ile Ser Gly Gly Ala Gly Leu Pro Ile Ala Ile Leu Ala	
85 90 95	
ggg gcg gcg ctc gtg att gct att ggg gat gct tgc tgt gcg tat cat	336
Gly Ala Ala Leu Val Ile Ala Ile Gly Asp Ala Cys Cys Ala Tyr His	
100 105 110	
aat tat caa tcg ata tgt cag caa aag gag cca tta caa acc gcc agt	384
Asn Tyr Gln Ser Ile Cys Gln Gln Lys Glu Pro Leu Gln Thr Ala Ser	
115 120 125	
gat agc gtt gct ctt gtg gtc agt gcg ctg gcc tta aaa tgt ggg gca	432
Asp Ser Val Ala Leu Val Val Ser Ala Leu Ala Leu Lys Cys Gly Ala	
130 135 140	
agt ctt aac tgc gct aac acc ctt gct aat tgt ctt tct tta tta ata	480
Ser Leu Asn Cys Ala Asn Thr Leu Ala Asn Cys Leu Ser Leu Leu Ile	
145 150 155 160	
cgt tca gga atc gct att tct atg ttg gtt tta ccc cta cag ttt cca	528
Arg Ser Gly Ile Ala Ile Ser Met Leu Val Leu Pro Leu Gln Phe Pro	
165 170 175	
ctg ccc gcg gct gaa aat att gcg gcc tct ttg gac atg ggg agt gta	576
Leu Pro Ala Ala Glu Asn Ile Ala Ala Ser Leu Asp Met Gly Ser Val	
180 185 190	
att acc tcc gtt agc ctg acg gcg ata ggt gcg gta ctg gat tat tgc	624
Ile Thr Ser Val Ser Leu Thr Ala Ile Gly Ala Val Leu Asp Tyr Cys	
195 200 205	
ctt gcc cgc ccc tct ggc gac gat cag gaa aat tct gtt gat gaa ctt	672
Leu Ala Arg Pro Ser Gly Asp Asp Gln Glu Asn Ser Val Asp Glu Leu	
210 215 220	
cat gcc gat ccc agt gtg tta ttg gcg gaa caa atg gca gcg ctc tgt	720
His Ala Asp Pro Ser Val Leu Leu Ala Glu Gln Met Ala Ala Leu Cys	
225 230 235 240	
caa tct gct act aca cct gca cct gca tta atg gac agt tct gat cat	768
Gln Ser Ala Thr Thr Pro Ala Pro Ala Leu Met Asp Ser Ser Asp His	
245 250 255	
aca tct cgg gga gaa cca tga	789
Thr Ser Arg Gly Glu Pro	
260	

<210> 15  
 <211> 262  
 <212> PRT

<213> Salmonella

<400> 15

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Met Lys Ile His Ile Pro Ser Ala Ala Ser Asn Ile Val Asp Gly Asn
 1              5              10              15

Ser Pro Pro Ser Asp Ile Gln Ala Lys Glu Val Ser Phe Pro Pro Pro
      20              25              30

Glu Ile Pro Ala Pro Gly Thr Pro Ala Ala Pro Val Leu Leu Thr Pro
      35              40              45

Glu Gln Ile Arg Gln Gln Arg Asp Tyr Ala Ile His Phe Met Gln Tyr
 50              55              60

Thr Ile Arg Ala Leu Gly Ala Thr Val Val Phe Gly Leu Ser Val Ala
 65              70              75              80

Ala Ala Val Ile Ser Gly Gly Ala Gly Leu Pro Ile Ala Ile Leu Ala
      85              90              95

Gly Ala Ala Leu Val Ile Ala Ile Gly Asp Ala Cys Cys Ala Tyr His
      100              105              110

Asn Tyr Gln Ser Ile Cys Gln Gln Lys Glu Pro Leu Gln Thr Ala Ser
      115              120              125

Asp Ser Val Ala Leu Val Val Ser Ala Leu Ala Leu Lys Cys Gly Ala
      130              135              140

Ser Leu Asn Cys Ala Asn Thr Leu Ala Asn Cys Leu Ser Leu Leu Ile
      145              150              155              160

Arg Ser Gly Ile Ala Ile Ser Met Leu Val Leu Pro Leu Gln Phe Pro
      165              170              175

Leu Pro Ala Ala Glu Asn Ile Ala Ala Ser Leu Asp Met Gly Ser Val
      180              185              190

Ile Thr Ser Val Ser Leu Thr Ala Ile Gly Ala Val Leu Asp Tyr Cys
      195              200              205

Leu Ala Arg Pro Ser Gly Asp Asp Gln Glu Asn Ser Val Asp Glu Leu
      210              215              220

His Ala Asp Pro Ser Val Leu Leu Ala Glu Gln Met Ala Ala Leu Cys
      225              230              235              240

Gln Ser Ala Thr Thr Pro Ala Pro Ala Leu Met Asp Ser Ser Asp His
      245              250              255

Thr Ser Arg Gly Glu Pro
      260
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<210> 16

<211> 690  
 <212> DNA  
 <213> Salmonella

<220>  
 <221> CDS  
 <222> (1)..(687)

<400> 16

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Met Lys Pro Val Ser Pro Asn Ala Gln Val Gly Gly Gln Arg Pro Val	
1 5 10 15	
aac gcg cct gag gaa tca cct cca tgt cct tca ttg cca cat ccg gaa	96
Asn Ala Pro Glu Glu Ser Pro Pro Cys Pro Ser Leu Pro His Pro Glu	
20 25 30	
acc aat atg gag agt ggt aga ata gga cct caa caa gga aaa gag cgg	144
Thr Asn Met Glu Ser Gly Arg Ile Gly Pro Gln Gln Gly Lys Glu Arg	
35 40 45	
gta ttg gcc gga ctt gcg aaa cga gtg ata gag tgt ttt cca aaa gaa	192
Val Leu Ala Gly Leu Ala Lys Arg Val Ile Glu Cys Phe Pro Lys Glu	
50 55 60	
att ttt agt tgg caa acg gtt att ttg ggc gga cag att tta tgc tgt	240
Ile Phe Ser Trp Gln Thr Val Ile Leu Gly Gly Gln Ile Leu Cys Cys	
65 70 75 80	
tcc gct gga ata gca tta aca gtg cta agt ggt gga ggc gcg ccg ctc	288
Ser Ala Gly Ile Ala Leu Thr Val Leu Ser Gly Gly Gly Ala Pro Leu	
85 90 95	
gta gcc ctg gca ggg att ggc ctt gct att gcc atc gcg gat gtc gcc	336
Val Ala Leu Ala Gly Ile Gly Leu Ala Ile Ala Ile Ala Asp Val Ala	
100 105 110	
tgt ctt atc tac cat cat aaa cat cat ttg cct atg gct cac gac agt	384
Cys Leu Ile Tyr His His Lys His His Leu Pro Met Ala His Asp Ser	
115 120 125	
ata ggc aat gcc gtt ttt tat att gct aat tgt ttc gcc aat caa cgc	432
Ile Gly Asn Ala Val Phe Tyr Ile Ala Asn Cys Phe Ala Asn Gln Arg	
130 135 140	
aaa agt atg gcg att gct aaa gcc gtc tcc ctg ggc ggt aga tta gcc	480
Lys Ser Met Ala Ile Ala Lys Ala Val Ser Leu Gly Gly Arg Leu Ala	
145 150 155 160	
tta acc gcg acg gta atg act cat tca tac tgg agt ggt agt ttg gga	528
Leu Thr Ala Thr Val Met Thr His Ser Tyr Trp Ser Gly Ser Leu Gly	
165 170 175	
cta cag cct cat tta tta gag cgt ctt aat gat att acc tat gga cta	576
Leu Gln Pro His Leu Leu Glu Arg Leu Asn Asp Ile Thr Tyr Gly Leu	
180 185 190	

atg agt ttt act cgc ttc ggt atg gat ggg atg gca atg acc ggt atg	624
Met Ser Phe Thr Arg Phe Gly Met Asp Gly Met Ala Met Thr Gly Met	
195 200 205	

cag gtc agc agc cca tta tat cgt ttg ctg gct cag gta acg cca gaa	672
Gln Val Ser Ser Pro Leu Tyr Arg Leu Leu Ala Gln Val Thr Pro Glu	
210 215 220	

caa cgt gcg ccg gag taa	690
Gln Arg Ala Pro Glu	
225	

<210> 17  
 <211> 229  
 <212> PRT  
 <213> Salmonella

<400> 17	
Met Lys Pro Val Ser Pro Asn Ala Gln Val Gly Gly Gln Arg Pro Val	
1 5 10 15	
Asn Ala Pro Glu Glu Ser Pro Pro Cys Pro Ser Leu Pro His Pro Glu	
20 25 30	
Thr Asn Met Glu Ser Gly Arg Ile Gly Pro Gln Gln Gly Lys Glu Arg	
35 40 45	
Val Leu Ala Gly Leu Ala Lys Arg Val Ile Glu Cys Phe Pro Lys Glu	
50 55 60	
Ile Phe Ser Trp Gln Thr Val Ile Leu Gly Gly Gln Ile Leu Cys Cys	
65 70 75 80	
Ser Ala Gly Ile Ala Leu Thr Val Leu Ser Gly Gly Gly Ala Pro Leu	
85 90 95	
Val Ala Leu Ala Gly Ile Gly Leu Ala Ile Ala Ile Ala Asp Val Ala	
100 105 110	
Cys Leu Ile Tyr His His Lys His His Leu Pro Met Ala His Asp Ser	
115 120 125	
Ile Gly Asn Ala Val Phe Tyr Ile Ala Asn Cys Phe Ala Asn Gln Arg	
130 135 140	
Lys Ser Met Ala Ile Ala Lys Ala Val Ser Leu Gly Gly Arg Leu Ala	
145 150 155 160	
Leu Thr Ala Thr Val Met Thr His Ser Tyr Trp Ser Gly Ser Leu Gly	
165 170 175	
Leu Gln Pro His Leu Leu Glu Arg Leu Asn Asp Ile Thr Tyr Gly Leu	
180 185 190	
Met Ser Phe Thr Arg Phe Gly Met Asp Gly Met Ala Met Thr Gly Met	
195 200 205	

Gln Val Ser Ser Pro Leu Tyr Arg Leu Leu Ala Gln Val Thr Pro Glu  
 210 215 220

Gln Arg Ala Pro Glu  
 225

<210> 18  
 <211> 474  
 <212> DNA  
 <213> Salmonella

<220>  
 <221> CDS  
 <222> (1) .. (471)

<400> 18  
 atg aaa aaa gac ccg acc cta caa cag gca cat gac acg atg cgg ttt 48  
 Met Lys Lys Asp Pro Thr Leu Gln Gln Ala His Asp Thr Met Arg Phe  
 1 5 10 15  
 ttc cgg cgt ggc ggc tcg ctg cgt atg ttg ttg gat gac gat gtt aca 96  
 Phe Arg Arg Gly Gly Ser Leu Arg Met Leu Leu Asp Asp Asp Val Thr  
 20 25 30  
 cag ccg ctt aat act ctg tat cgc tat gcc acg cag ctt atg gag gta 144  
 Gln Pro Leu Asn Thr Leu Tyr Arg Tyr Ala Thr Gln Leu Met Glu Val  
 35 40 45  
 aaa gaa ttc gcc ggc gca gcg cga ctt ttt caa ttg ctg acg ata tat 192  
 Lys Glu Phe Ala Gly Ala Ala Arg Leu Phe Gln Leu Leu Thr Ile Tyr  
 50 55 60  
 gat gcc tgg tca ttt gac tac tgg ttt cgg tta ggg gaa tgc tgc cag 240  
 Asp Ala Trp Ser Phe Asp Tyr Trp Phe Arg Leu Gly Glu Cys Cys Gln  
 65 70 75 80  
 gct caa aaa cat tgg ggg gaa gcg ata tac gct tat gga cgc gcg gca 288  
 Ala Gln Lys His Trp Gly Glu Ala Ile Tyr Ala Tyr Gly Arg Ala Ala  
 85 90 95  
 caa att aag att gat gcg ccg cag gcg cca tgg gcc gca gcg gaa tgc 336  
 Gln Ile Lys Ile Asp Ala Pro Gln Ala Pro Trp Ala Ala Ala Glu Cys  
 100 105 110  
 tat ctc gcg tgt gat aac gtc tgt tat gca atc aaa gcg tta aag gcc 384  
 Tyr Leu Ala Cys Asp Asn Val Cys Tyr Ala Ile Lys Ala Leu Lys Ala  
 115 120 125  
 gtg gtg cgt att tgc ggc gag gtc agt gaa cat caa att ctc cga cag 432  
 Val Val Arg Ile Cys Gly Glu Val Ser Glu His Gln Ile Leu Arg Gln  
 130 135 140  
 cgt gca gaa aag atg tta cag caa ctt tct gac agg agc taa 474  
 Arg Ala Glu Lys Met Leu Gln Gln Leu Ser Asp Arg Ser

145

150

155

&lt;210&gt; 19

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Salmonella

&lt;400&gt; 19

Met	Lys	Lys	Asp	Pro	Thr	Leu	Gln	Gln	Ala	His	Asp	Thr	Met	Arg	Phe
1				5					10					15	

Phe	Arg	Arg	Gly	Gly	Ser	Leu	Arg	Met	Leu	Leu	Asp	Asp	Asp	Val	Thr
			20					25					30		

Gln	Pro	Leu	Asn	Thr	Leu	Tyr	Arg	Tyr	Ala	Thr	Gln	Leu	Met	Glu	Val
		35					40					45			

Lys	Glu	Phe	Ala	Gly	Ala	Ala	Arg	Leu	Phe	Gln	Leu	Leu	Thr	Ile	Tyr
	50					55					60				

Asp	Ala	Trp	Ser	Phe	Asp	Tyr	Trp	Phe	Arg	Leu	Gly	Glu	Cys	Cys	Gln
65					70					75					80

Ala	Gln	Lys	His	Trp	Gly	Glu	Ala	Ile	Tyr	Ala	Tyr	Gly	Arg	Ala	Ala
				85					90					95	

Gln	Ile	Lys	Ile	Asp	Ala	Pro	Gln	Ala	Pro	Trp	Ala	Ala	Ala	Glu	Cys
			100					105					110		

Tyr	Leu	Ala	Cys	Asp	Asn	Val	Cys	Tyr	Ala	Ile	Lys	Ala	Leu	Lys	Ala
		115					120					125			

Val	Val	Arg	Ile	Cys	Gly	Glu	Val	Ser	Glu	His	Gln	Ile	Leu	Arg	Gln
	130					135					140				

Arg	Ala	Glu	Lys	Met	Leu	Gln	Gln	Leu	Ser	Asp	Arg	Ser
145					150					155		

&lt;210&gt; 20

&lt;211&gt; 435

&lt;212&gt; DNA

&lt;213&gt; Salmonella

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(432)

&lt;400&gt; 20

atg	atg	atg	aaa	gaa	gat	cag	aaa	aat	aaa	ata	ccc	gaa	gac	att	ctg	48
Met	Met	Met	Lys	Glu	Asp	Gln	Lys	Asn	Lys	Ile	Pro	Glu	Asp	Ile	Leu	
1				5					10					15		

aaa	cag	cta	tta	tcc	gtt	gat	ccg	gaa	acc	gtt	tat	gcc	agt	ggg	tac	96
Lys	Gln	Leu	Leu	Ser	Val	Asp	Pro	Glu	Thr	Val	Tyr	Ala	Ser	Gly	Tyr	

20										25					30					
gcc tca tgg cag gag ggg gat tat tcg cgc gcc gta atc gat ttt agt	144																			
Ala Ser Trp Gln Glu Gly Asp Tyr Ser Arg Ala Val Ile Asp Phe Ser																				
35 40 45																				
tgg ctg gtg atg gcc cag cca tgg agt tgg cgt gcc cat att gca ttg	192																			
Trp Leu Val Met Ala Gln Pro Trp Ser Trp Arg Ala His Ile Ala Leu																				
50 55 60																				
gct ggc acc tgg atg atg ctt aaa gaa tac acg acg gcc att aat ttc	240																			
Ala Gly Thr Trp Met Met Leu Lys Glu Tyr Thr Thr Ala Ile Asn Phe																				
65 70 75 80																				
tat gga cat gcc ttg atg ctg gat gcc agc cat cca gaa ccg gtt tac	288																			
Tyr Gly His Ala Leu Met Leu Asp Ala Ser His Pro Glu Pro Val Tyr																				
85 90 95																				
caa acg ggc gtc tgt ctc aaa atg atg ggg gaa ccc ggg ttg gcg aga	336																			
Gln Thr Gly Val Cys Leu Lys Met Met Gly Glu Pro Gly Leu Ala Arg																				
100 105 110																				
gag gct ttt caa acc gca atc aag atg agt tat gcg gat gcc tca tgg	384																			
Glu Ala Phe Gln Thr Ala Ile Lys Met Ser Tyr Ala Asp Ala Ser Trp																				
115 120 125																				
agt gag att cgc cag aat gcg caa ata atg gtt gat act ctt att gct	432																			
Ser Glu Ile Arg Gln Asn Ala Gln Ile Met Val Asp Thr Leu Ile Ala																				
130 135 140																				
taa	435																			

<210> 21  
 <211> 144  
 <212> PRT  
 <213> Salmonella

<400> 21  
 Met Met Met Lys Glu Asp Gln Lys Asn Lys Ile Pro Glu Asp Ile Leu  
 1 5 10 15  
 Lys Gln Leu Leu Ser Val Asp Pro Glu Thr Val Tyr Ala Ser Gly Tyr  
 20 25 30  
 Ala Ser Trp Gln Glu Gly Asp Tyr Ser Arg Ala Val Ile Asp Phe Ser  
 35 40 45  
 Trp Leu Val Met Ala Gln Pro Trp Ser Trp Arg Ala His Ile Ala Leu  
 50 55 60  
 Ala Gly Thr Trp Met Met Leu Lys Glu Tyr Thr Thr Ala Ile Asn Phe  
 65 70 75 80  
 Tyr Gly His Ala Leu Met Leu Asp Ala Ser His Pro Glu Pro Val Tyr  
 85 90 95

Gln	Thr	Gly	Val	Cys	Leu	Lys	Met	Met	Gly	Glu	Pro	Gly	Leu	Ala	Arg
			100					105					110		
Glu	Ala	Phe	Gln	Thr	Ala	Ile	Lys	Met	Ser	Tyr	Ala	Asp	Ala	Ser	Trp
		115					120					125			
Ser	Glu	Ile	Arg	Gln	Asn	Ala	Gln	Ile	Met	Val	Asp	Thr	Leu	Ile	Ala
	130					135					140				

<210> 22  
 <211> 1212  
 <212> DNA  
 <213> Salmonella

<220>  
 <221> CDS  
 <222> (1)..(1209)

<400> 22																
atg	gca	tat	ctc	atg	gtt	aat	cca	aag	agt	tcc	tgg	aaa	ata	cgt	ttt	48
Met	Ala	Tyr	Leu	Met	Val	Asn	Pro	Lys	Ser	Ser	Trp	Lys	Ile	Arg	Phe	
1					5				10					15		
tta	ggt	cac	gtt	tta	caa	ggc	cgg	gaa	gta	tgg	ctg	aat	gaa	ggt	aac	96
Leu	Gly	His	Val	Leu	Gln	Gly	Arg	Glu	Val	Trp	Leu	Asn	Glu	Gly	Asn	
			20					25					30			
ctg	tca	ctg	ggg	gag	aag	gga	tgc	gat	att	tgt	att	ccg	ctg	gct	ata	144
Leu	Ser	Leu	Gly	Glu	Lys	Gly	Cys	Asp	Ile	Cys	Ile	Pro	Leu	Ala	Ile	
		35				40						45				
aat	gaa	aaa	att	att	ctg	aga	gaa	cag	gca	gat	agt	tta	ttt	gtt	gat	192
Asn	Glu	Lys	Ile	Ile	Leu	Arg	Glu	Gln	Ala	Asp	Ser	Leu	Phe	Val	Asp	
	50					55					60					
gcc	ggg	aaa	gcc	aga	gtt	aga	gtt	aat	ggc	cgc	aga	ttt	aat	cca	aat	240
Ala	Gly	Lys	Ala	Arg	Val	Arg	Val	Asn	Gly	Arg	Arg	Phe	Asn	Pro	Asn	
65					70				75					80		
aag	ccg	cta	cca	tcc	agt	ggg	gtt	ttg	cag	gtt	gcg	gga	gtg	gct	atc	288
Lys	Pro	Leu	Pro	Ser	Ser	Gly	Val	Leu	Gln	Val	Ala	Gly	Val	Ala	Ile	
				85				90						95		
gcg	ttt	ggt	aaa	cag	gat	tgt	gaa	ctt	gct	gat	tat	caa	ata	ccc	gtt	336
Ala	Phe	Gly	Lys	Gln	Asp	Cys	Glu	Leu	Ala	Asp	Tyr	Gln	Ile	Pro	Val	
			100				105					110				
tcc	aga	tca	ggg	tac	tgg	tgg	ttg	gct	ggc	gta	ttc	ttg	att	ttc	atc	384
Ser	Arg	Ser	Gly	Tyr	Trp	Trp	Leu	Ala	Gly	Val	Phe	Leu	Ile	Phe	Ile	
		115					120					125				
ggt	gga	atg	ggt	gtc	ctg	tta	agt	att	agt	ggt	cag	cct	gaa	acg	gta	432
Gly	Gly	Met	Gly	Val	Leu	Leu	Ser	Ile	Ser	Gly	Gln	Pro	Glu	Thr	Val	
	130					135					140					



aat gac tta cct ttg cgg gtt aag ttt tta tta gac aaa agc aat att	480
Asn Asp Leu Pro Leu Arg Val Lys Phe Leu Leu Asp Lys Ser Asn Ile	
145 150 155 160	
cat tat gtg cgg gcg caa tgg aaa gaa gat ggc agc ctg cag ttg tcc	528
His Tyr Val Arg Ala Gln Trp Lys Glu Asp Gly Ser Leu Gln Leu Ser	
165 170 175	
ggt tat tgc tcg tca agc gaa cag atg caa aag gtg aga gcg act ctc	576
Gly Tyr Cys Ser Ser Ser Glu Gln Met Gln Lys Val Arg Ala Thr Leu	
180 185 190	
gaa tca tgg ggg gtc atg tat cgg gat ggt gta atc tgt gat gac tta	624
Glu Ser Trp Gly Val Met Tyr Arg Asp Gly Val Ile Cys Asp Asp Leu	
195 200 205	
ttg gta cga gaa gtg cag gat gtt ttg ata aaa atg ggt tac ccg cat	672
Leu Val Arg Glu Val Gln Asp Val Leu Ile Lys Met Gly Tyr Pro His	
210 215 220	
gct gaa gta tcc agc gaa ggg ccg ggg agc gtg tta att cat gat gat	720
Ala Glu Val Ser Ser Glu Gly Pro Gly Ser Val Leu Ile His Asp Asp	
225 230 235 240	
ata caa atg gat cag caa tgg cgc aag gtt caa cca tta ctt gca gat	768
Ile Gln Met Asp Gln Gln Trp Arg Lys Val Gln Pro Leu Leu Ala Asp	
245 250 255	
att ccc ggg tta ttg cac tgg cag att agt cac tct cat cag tct cag	816
Ile Pro Gly Leu Leu His Trp Gln Ile Ser His Ser His Gln Ser Gln	
260 265 270	
ggg gat gat att att tct gcg ata ata gag aac ggt tta gtg ggg ctt	864
Gly Asp Asp Ile Ile Ser Ala Ile Ile Glu Asn Gly Leu Val Gly Leu	
275 280 285	
gtc aat gtt agc cca atg cgg cgc tct ttt gtt atc agt ggt gta ctg	912
Val Asn Val Ser Pro Met Arg Arg Ser Phe Val Ile Ser Gly Val Leu	
290 295 300	
gat gaa tct cat caa cgc att ttg caa gaa acg tta gca gca tta aag	960
Asp Glu Ser His Gln Arg Ile Leu Gln Glu Thr Leu Ala Ala Leu Lys	
305 310 315 320	
aaa aag gat ccc gct ctt tct tta att tat cag gat att gcg cct tcc	1008
Lys Lys Asp Pro Ala Leu Ser Leu Ile Tyr Gln Asp Ile Ala Pro Ser	
325 330 335	
cat gat gaa agc aag tat ctg cct gcg cca gtg gct ggc ttt gta cag	1056
His Asp Glu Ser Lys Tyr Leu Pro Ala Pro Val Ala Gly Phe Val Gln	
340 345 350	
agt cgc cat ggt aat tac tta tta ctg acg aat aaa gag cgt tta cgt	1104
Ser Arg His Gly Asn Tyr Leu Leu Leu Thr Asn Lys Glu Arg Leu Arg	
355 360 365	
gta ggg gca ttg tta ccc aat ggg gga gaa att gtc cat ctg agt gcc	1152

Val Gly Ala Leu Leu Pro Asn Gly Gly Glu Ile Val His Leu Ser Ala  
 370 375 380

gat gtg gta acg att aaa cat tat gat act ttg att aac tat cca tta 1200  
 Asp Val Val Thr Ile Lys His Tyr Asp Thr Leu Ile Asn Tyr Pro Leu  
 385 390 395 400

gat ttt aag tga 1212  
 Asp Phe Lys

<210> 23  
 <211> 403  
 <212> PRT  
 <213> Salmonella

<400> 23  
 Met Ala Tyr Leu Met Val Asn Pro Lys Ser Ser Trp Lys Ile Arg Phe  
 1 5 10 15

Leu Gly His Val Leu Gln Gly Arg Glu Val Trp Leu Asn Glu Gly Asn  
 20 25 30

Leu Ser Leu Gly Glu Lys Gly Cys Asp Ile Cys Ile Pro Leu Ala Ile  
 35 40 45

Asn Glu Lys Ile Ile Leu Arg Glu Gln Ala Asp Ser Leu Phe Val Asp  
 50 55 60

Ala Gly Lys Ala Arg Val Arg Val Asn Gly Arg Arg Phe Asn Pro Asn  
 65 70 75 80

Lys Pro Leu Pro Ser Ser Gly Val Leu Gln Val Ala Gly Val Ala Ile  
 85 90 95

Ala Phe Gly Lys Gln Asp Cys Glu Leu Ala Asp Tyr Gln Ile Pro Val  
 100 105 110

Ser Arg Ser Gly Tyr Trp Trp Leu Ala Gly Val Phe Leu Ile Phe Ile  
 115 120 125

Gly Gly Met Gly Val Leu Leu Ser Ile Ser Gly Gln Pro Glu Thr Val  
 130 135 140

Asn Asp Leu Pro Leu Arg Val Lys Phe Leu Leu Asp Lys Ser Asn Ile  
 145 150 155 160

His Tyr Val Arg Ala Gln Trp Lys Glu Asp Gly Ser Leu Gln Leu Ser  
 165 170 175

Gly Tyr Cys Ser Ser Ser Glu Gln Met Gln Lys Val Arg Ala Thr Leu  
 180 185 190

Glu Ser Trp Gly Val Met Tyr Arg Asp Gly Val Ile Cys Asp Asp Leu  
 195 200 205

Leu Val Arg Glu Val Gln Asp Val Leu Ile Lys Met Gly Tyr Pro His

210	215	220	
Ala Glu Val Ser Ser Glu Gly Pro Gly Ser Val Leu Ile His Asp Asp			
225	230	235	240
Ile Gln Met Asp Gln Gln Trp Arg Lys Val Gln Pro Leu Leu Ala Asp			
	245	250	255
Ile Pro Gly Leu Leu His Trp Gln Ile Ser His Ser His Gln Ser Gln			
	260	265	270
Gly Asp Asp Ile Ile Ser Ala Ile Ile Glu Asn Gly Leu Val Gly Leu			
	275	280	285
Val Asn Val Ser Pro Met Arg Arg Ser Phe Val Ile Ser Gly Val Leu			
	290	295	300
Asp Glu Ser His Gln Arg Ile Leu Gln Glu Thr Leu Ala Ala Leu Lys			
305	310	315	320
Lys Lys Asp Pro Ala Leu Ser Leu Ile Tyr Gln Asp Ile Ala Pro Ser			
	325	330	335
His Asp Glu Ser Lys Tyr Leu Pro Ala Pro Val Ala Gly Phe Val Gln			
	340	345	350
Ser Arg His Gly Asn Tyr Leu Leu Leu Thr Asn Lys Glu Arg Leu Arg			
	355	360	365
Val Gly Ala Leu Leu Pro Asn Gly Gly Glu Ile Val His Leu Ser Ala			
	370	375	380
Asp Val Val Thr Ile Lys His Tyr Asp Thr Leu Ile Asn Tyr Pro Leu			
385	390	395	400
Asp Phe Lys			

<210> 24  
 <211> 243  
 <212> DNA  
 <213> Salmonella

<220>  
 <221> CDS  
 <222> (1)..(240)

<400> 24	
atg aca act ttg acc cgg tta gaa gat ttg ctg ctt cat tcg cgt gaa	48
Met Thr Thr Leu Thr Arg Leu Glu Asp Leu Leu Leu His Ser Arg Glu	
1 5 10 15	
gag gcc aaa ggc ata att tta caa tta agg gct gcc cgg aaa cag tta	96
Glu Ala Lys Gly Ile Ile Leu Gln Leu Arg Ala Ala Arg Lys Gln Leu	
20 25 30	

gaa gag aac aac ggc aag tta cag gat ccg cag caa tat cag caa aac	144
Glu Glu Asn Asn Gly Lys Leu Gln Asp Pro Gln Gln Tyr Gln Gln Asn	
35 40 45	
acc tta ttg ctt gaa gcg atc gag cag gcc gaa aat atc atc aac att	192
Thr Leu Leu Leu Glu Ala Ile Glu Gln Ala Glu Asn Ile Ile Asn Ile	
50 55 60	
att tat tat cgt tac cat aac agc gca ctt gta gtg agt gag caa gag	240
Ile Tyr Tyr Arg Tyr His Asn Ser Ala Leu Val Val Ser Glu Gln Glu	
65 70 75 80	
taa	243

<210> 25  
 <211> 80  
 <212> PRT  
 <213> Salmonella

<400> 25	
Met Thr Thr Leu Thr Arg Leu Glu Asp Leu Leu Leu His Ser Arg Glu	
1 5 10 15	
Glu Ala Lys Gly Ile Ile Leu Gln Leu Arg Ala Ala Arg Lys Gln Leu	
20 25 30	
Glu Glu Asn Asn Gly Lys Leu Gln Asp Pro Gln Gln Tyr Gln Gln Asn	
35 40 45	
Thr Leu Leu Leu Glu Ala Ile Glu Gln Ala Glu Asn Ile Ile Asn Ile	
50 55 60	
Ile Tyr Tyr Arg Tyr His Asn Ser Ala Leu Val Val Ser Glu Gln Glu	
65 70 75 80	

<210> 26  
 <211> 216  
 <212> DNA  
 <213> Salmonella

<220>  
 <221> CDS  
 <222> (1)..(213)

<400> 26	
atg gat att gca caa tta gtg gat atg ctc tcc cac atg gcg cac cag	48
Met Asp Ile Ala Gln Leu Val Asp Met Leu Ser His Met Ala His Gln	
1 5 10 15	
gca ggc cag gcc att aat gac aaa atg aat ggt aat gat ttg ctc aac	96
Ala Gly Gln Ala Ile Asn Asp Lys Met Asn Gly Asn Asp Leu Leu Asn	
20 25 30	

cca gaa tcg atg att aaa gcg caa ttt gcc tta cag cag tat tct aca	144
Pro Glu Ser Met Ile Lys Ala Gln Phe Ala Leu Gln Gln Tyr Ser Thr	
35 40 45	

ttt att aat tac gaa agt tca ctg atc aaa atg atc aag gat atg ctt	192
Phe Ile Asn Tyr Glu Ser Ser Leu Ile Lys Met Ile Lys Asp Met Leu	
50 55 60	

agt gga atc att gct aaa atc tga	216
Ser Gly Ile Ile Ala Lys Ile	
65 70	

<210> 27  
 <211> 71  
 <212> PRT  
 <213> Salmonella

<400> 27	
Met Asp Ile Ala Gln Leu Val Asp Met Leu Ser His Met Ala His Gln	
1 5 10 15	
Ala Gly Gln Ala Ile Asn Asp Lys Met Asn Gly Asn Asp Leu Leu Asn	
20 25 30	
Pro Glu Ser Met Ile Lys Ala Gln Phe Ala Leu Gln Gln Tyr Ser Thr	
35 40 45	
Phe Ile Asn Tyr Glu Ser Ser Leu Ile Lys Met Ile Lys Asp Met Leu	
50 55 60	
Ser Gly Ile Ile Ala Lys Ile	
65 70	

<210> 28  
 <211> 228  
 <212> DNA  
 <213> Salmonella

<220>  
 <221> CDS  
 <222> (1)..(225)

<400> 28	
atg ttt gcg ggc gtt aac cat agc ctg att tcc cag gta cat gcg atg	48
Met Phe Ala Gly Val Asn His Ser Leu Ile Ser Gln Val His Ala Met	
1 5 10 15	
tta cca gcg cta acg gtt att gtt ccg gat aaa aaa tta cag ttg gta	96
Leu Pro Ala Leu Thr Val Ile Val Pro Asp Lys Lys Leu Gln Leu Val	
20 25 30	
tgt ctg gca tta ttg ttg gcg ggt tta aat gag ccg cta aaa gcc gcg	144
Cys Leu Ala Leu Leu Leu Ala Gly Leu Asn Glu Pro Leu Lys Ala Ala	
35 40 45	

aaa att tta tcg gat ata gat ttg cca gag gct atg gcg ctg cgt ctg	192
Lys Ile Leu Ser Asp Ile Asp Leu Pro Glu Ala Met Ala Leu Arg Leu	
50 55 60	

tta ttt cct gca cca aat gag ggg ttt gaa aat tga	228
Leu Phe Pro Ala Pro Asn Glu Gly Phe Glu Asn	
65 70 75	

<210> 29  
 <211> 75  
 <212> PRT  
 <213> Salmonella

<400> 29	
Met Phe Ala Gly Val Asn His Ser Leu Ile Ser Gln Val His Ala Met	
1 5 10 15	
Leu Pro Ala Leu Thr Val Ile Val Pro Asp Lys Lys Leu Gln Leu Val	
20 25 30	
Cys Leu Ala Leu Leu Leu Ala Gly Leu Asn Glu Pro Leu Lys Ala Ala	
35 40 45	
Lys Ile Leu Ser Asp Ile Asp Leu Pro Glu Ala Met Ala Leu Arg Leu	
50 55 60	
Leu Phe Pro Ala Pro Asn Glu Gly Phe Glu Asn	
65 70 75	

<210> 30  
 <211> 249  
 <212> DNA  
 <213> Salmonella

<220>  
 <221> CDS  
 <222> (1)..(246)

<400> 30	
atg agc gta gtg cct gta agc act caa tct tat gta aag tcc tct gca	48
Met Ser Val Val Pro Val Ser Thr Gln Ser Tyr Val Lys Ser Ser Ala	
1 5 10 15	
gaa ccg agc cag gag caa att aat ttt ttt gaa caa ttg ctg aaa gat	96
Glu Pro Ser Gln Glu Gln Ile Asn Phe Glu Gln Leu Leu Lys Asp	
20 25 30	
gaa gca tcc acc agt aac gcc agt gct tta tta ccg cag gtt atg ttg	144
Glu Ala Ser Thr Ser Asn Ala Ser Ala Leu Leu Pro Gln Val Met Leu	
35 40 45	
acc aga caa atg gat tat atg cag tta acg gta ggc gtc gat tat ctt	192
Thr Arg Gln Met Asp Tyr Met Gln Leu Thr Val Gly Val Asp Tyr Leu	

50	55	60	
gcc aga ata tca ggc gca gca tcg caa gcg ctt aat aag ctg gat aac	240		
Ala Arg Ile Ser Gly Ala Ala Ser Gln Ala Leu Asn Lys Leu Asp Asn			
65 70 75 80			

atg gca tga	249
Met Ala	

<210> 31  
 <211> 82  
 <212> PRT  
 <213> Salmonella

<400> 31	
Met Ser Val Val Pro Val Ser Thr Gln Ser Tyr Val Lys Ser Ser Ala	
1 5 10 15	
Glu Pro Ser Gln Glu Gln Ile Asn Phe Phe Glu Gln Leu Leu Lys Asp	
20 25 30	
Glu Ala Ser Thr Ser Asn Ala Ser Ala Leu Leu Pro Gln Val Met Leu	
35 40 45	
Thr Arg Gln Met Asp Tyr Met Gln Leu Thr Val Gly Val Asp Tyr Leu	
50 55 60	
Ala Arg Ile Ser Gly Ala Ala Ser Gln Ala Leu Asn Lys Leu Asp Asn	
65 70 75 80	
Met Ala	

<210> 32  
 <211> 750  
 <212> DNA  
 <213> Salmonella

<220>  
 <221> CDS  
 <222> (1)..(747)

<400> 32	
atg aag gtt cat cgt ata gta ttt ctt act gtc ctt acg ttc ttt ctt	48
Met Lys Val His Arg Ile Val Phe Leu Thr Val Leu Thr Phe Phe Leu	
1 5 10 15	
acg gca tgt gat gtg gat ctt tat cgc tca ttg cca gaa gat gaa gcg	96
Thr Ala Cys Asp Val Asp Leu Tyr Arg Ser Leu Pro Glu Asp Glu Ala	
20 25 30	
aat caa atg ctg gca tta ctt atg cag cat cat att gat gcg gaa aaa	144
Asn Gln Met Leu Ala Leu Leu Met Gln His His Ile Asp Ala Glu Lys	
35 40 45	

aaa cag gaa gag gat ggt gta acc tta cgt gtc gag cag tcg cag ttt	192
Lys Gln Glu Glu Asp Gly Val Thr Leu Arg Val Glu Gln Ser Gln Phe	
50 55 60	
att aat gcg gtt gag cta ctt aga ctt aac ggt tat ccg cat agg cag	240
Ile Asn Ala Val Glu Leu Leu Arg Leu Asn Gly Tyr Pro His Arg Gln	
65 70 75 80	
ttt aca acg gcg gat aag atg ttt ccg gct aat cag tta gtg gta tca	288
Phe Thr Thr Ala Asp Lys Met Phe Pro Ala Asn Gln Leu Val Val Ser	
85 90 95	
ccc cag gaa gaa cag cag aag att aat ttt tta aaa gaa caa aga att	336
Pro Gln Glu Glu Gln Gln Lys Ile Asn Phe Leu Lys Glu Gln Arg Ile	
100 105 110	
gaa gga atg ctg agt cag atg gag ggc gtg att aat gca aaa gtg acc	384
Glu Gly Met Leu Ser Gln Met Glu Gly Val Ile Asn Ala Lys Val Thr	
115 120 125	
att gcg cta ccg act tat gat gag gga agt aac gct tct ccg agc tca	432
Ile Ala Leu Pro Thr Tyr Asp Glu Gly Ser Asn Ala Ser Pro Ser Ser	
130 135 140	
gtt gcc gta ttt ata aaa tat tca cct cag gtc aat atg gag gcc ttt	480
Val Ala Val Phe Ile Lys Tyr Ser Pro Gln Val Asn Met Glu Ala Phe	
145 150 155 160	
cgg gta aaa att aaa gat tta ata gag atg tca atc cct ggg ttg caa	528
Arg Val Lys Ile Lys Asp Leu Ile Glu Met Ser Ile Pro Gly Leu Gln	
165 170 175	
tac agt aag att agt atc ttg atg cag cct gct gaa ttc aga atg gta	576
Tyr Ser Lys Ile Ser Ile Leu Met Gln Pro Ala Glu Phe Arg Met Val	
180 185 190	
gct gac gta ccc gcg aga caa aca ttc tgg att atg gac gtt atc aac	624
Ala Asp Val Pro Ala Arg Gln Thr Phe Trp Ile Met Asp Val Ile Asn	
195 200 205	
gcc aat aaa ggg aag gtg gtg aag tgg ttg atg aaa tac cct tat ccg	672
Ala Asn Lys Gly Lys Val Val Lys Trp Leu Met Lys Tyr Pro Tyr Pro	
210 215 220	
ttg atg tta tcg ttg aca gga ctg tta tta gga gtg ggc atc ctg atc	720
Leu Met Leu Ser Leu Thr Gly Leu Leu Leu Gly Val Gly Ile Leu Ile	
225 230 235 240	
ggc tat ttt tgc ctg aga cgc cgt ttt tga	750
Gly Tyr Phe Cys Leu Arg Arg Arg Phe	
245	

<210> 33  
 <211> 249  
 <212> PRT



<213> Salmonella

<400> 33

Met	Lys	Val	His	Arg	Ile	Val	Phe	Leu	Thr	Val	Leu	Thr	Phe	Phe	Leu	
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Thr	Ala	Cys	Asp	Val	Asp	Leu	Tyr	Arg	Ser	Leu	Pro	Glu	Asp	Glu	Ala	
			20					25					30			
Asn	Gln	Met	Leu	Ala	Leu	Leu	Met	Gln	His	His	Ile	Asp	Ala	Glu	Lys	
		35					40					45				
Lys	Gln	Glu	Glu	Asp	Gly	Val	Thr	Leu	Arg	Val	Glu	Gln	Ser	Gln	Phe	
	50					55					60					
Ile	Asn	Ala	Val	Glu	Leu	Leu	Arg	Leu	Asn	Gly	Tyr	Pro	His	Arg	Gln	
65					70					75					80	
Phe	Thr	Thr	Ala	Asp	Lys	Met	Phe	Pro	Ala	Asn	Gln	Leu	Val	Val	Ser	
				85					90					95		
Pro	Gln	Glu	Glu	Gln	Gln	Lys	Ile	Asn	Phe	Leu	Lys	Glu	Gln	Arg	Ile	
			100					105					110			
Glu	Gly	Met	Leu	Ser	Gln	Met	Glu	Gly	Val	Ile	Asn	Ala	Lys	Val	Thr	
		115					120					125				
Ile	Ala	Leu	Pro	Thr	Tyr	Asp	Glu	Gly	Ser	Asn	Ala	Ser	Pro	Ser	Ser	
	130					135					140					
Val	Ala	Val	Phe	Ile	Lys	Tyr	Ser	Pro	Gln	Val	Asn	Met	Glu	Ala	Phe	
145					150					155					160	
Arg	Val	Lys	Ile	Lys	Asp	Leu	Ile	Glu	Met	Ser	Ile	Pro	Gly	Leu	Gln	
				165					170					175		
Tyr	Ser	Lys	Ile	Ser	Ile	Leu	Met	Gln	Pro	Ala	Glu	Phe	Arg	Met	Val	
			180					185					190			
Ala	Asp	Val	Pro	Ala	Arg	Gln	Thr	Phe	Trp	Ile	Met	Asp	Val	Ile	Asn	
		195					200					205				
Ala	Asn	Lys	Gly	Lys	Val	Val	Lys	Trp	Leu	Met	Lys	Tyr	Pro	Tyr	Pro	
	210					215					220					
Leu	Met	Leu	Ser	Leu	Thr	Gly	Leu	Leu	Leu	Gly	Val	Gly	Ile	Leu	Ile	
225					230					235				240		
Gly	Tyr	Phe	Cys	Leu	Arg	Arg	Arg	Phe								
				245												

<210> 34

<211> 2763

<212> DNA

<213> Salmonella

<220>

<221> CDS

<222> (1) .. (2760)

<400> 34

atg aat ttg ctc aat ctc aag aat acg ctg caa aca tct tta gta atc	48
Met Asn Leu Leu Asn Leu Lys Asn Thr Leu Gln Thr Ser Leu Val Ile	
1 5 10 15	
agg cta act ttt tta ttt tta tta aca aca ata att att tgg ctg cta	96
Arg Leu Thr Phe Leu Phe Leu Leu Thr Thr Ile Ile Ile Trp Leu Leu	
20 25 30	
tct gtg ctt acc gca gct tat ata tca atg gtt cag aaa cgg cag cat	144
Ser Val Leu Thr Ala Ala Tyr Ile Ser Met Val Gln Lys Arg Gln His	
35 40 45	
ata ata gag gat tta tcc gtt cta tcc gag atg aat att gta cta agc	192
Ile Ile Glu Asp Leu Ser Val Leu Ser Glu Met Asn Ile Val Leu Ser	
50 55 60	
aat caa cgg ttt gaa gaa gct gaa cgt gac gct aaa aat tta atg tat	240
Asn Gln Arg Phe Glu Glu Ala Glu Arg Asp Ala Lys Asn Leu Met Tyr	
65 70 75 80	
caa tgc tca tta gcg act gag att cat cat aac gat att ttc cct gag	288
Gln Cys Ser Leu Ala Thr Glu Ile His His Asn Asp Ile Phe Pro Glu	
85 90 95	
gtg agc cgg cat cta tct gtc ggt cct tca aat tgc acg ccg acg cta	336
Val Ser Arg His Leu Ser Val Gly Pro Ser Asn Cys Thr Pro Thr Leu	
100 105 110	
aac gga gag aag cac cgt ctc ttt ctg cag tcc tct gat atc gat gaa	384
Asn Gly Glu Lys His Arg Leu Phe Leu Gln Ser Ser Asp Ile Asp Glu	
115 120 125	
aat agc ttt cgt cgc gat agt ttt att ctt aat cat aaa aat gag att	432
Asn Ser Phe Arg Arg Asp Ser Phe Ile Leu Asn His Lys Asn Glu Ile	
130 135 140	
tcg tta tta tct act gat aac cct tca gat tat tca act cta cag cct	480
Ser Leu Leu Ser Thr Asp Asn Pro Ser Asp Tyr Ser Thr Leu Gln Pro	
145 150 155 160	
tta acg cga aaa agc ttt cct tta tac cca acc cat gcc ggg ttt tac	528
Leu Thr Arg Lys Ser Phe Pro Leu Tyr Pro Thr His Ala Gly Phe Tyr	
165 170 175	
tgg agt gaa cca gaa tac ata aac ggc aaa gga tgg cac gct tcc gtt	576
Trp Ser Glu Pro Glu Tyr Ile Asn Gly Lys Gly Trp His Ala Ser Val	
180 185 190	
gcg gtt gcc gat cag caa ggc gta ttt ttt gag gtg acg gtt aaa ctt	624
Ala Val Ala Asp Gln Gln Gly Val Phe Phe Glu Val Thr Val Lys Leu	
195 200 205	

ccc gat ctc att act aag agc cac ctg cca tta gat gat agt att cga	672
Pro Asp Leu Ile Thr Lys Ser His Leu Pro Leu Asp Asp Ser Ile Arg	
210 215 220	
gta tgg ctg gat caa aac aac cac tta ttg ccg ttt tca tac atc ccg	720
Val Trp Leu Asp Gln Asn Asn His Leu Leu Pro Phe Ser Tyr Ile Pro	
225 230 235 240	
caa aaa ata cgt aca cag tta gaa aat gta acg ctg cat gat gga tgg	768
Gln Lys Ile Arg Thr Gln Leu Glu Asn Val Thr Leu His Asp Gly Trp	
245 250 255	
cag caa att ccc gga ttt ctg ata tta cgc aca acc ttg cat ggc ccc	816
Gln Gln Ile Pro Gly Phe Leu Ile Leu Arg Thr Thr Leu His Gly Pro	
260 265 270	
gga tgg agt ctg gtt acg ctg tac cca tac ggt aat cta cat aat cgc	864
Gly Trp Ser Leu Val Thr Leu Tyr Pro Tyr Gly Asn Leu His Asn Arg	
275 280 285	
atc tta aaa att atc ctt caa caa atc ccc ttt aca tta aca gca ttg	912
Ile Leu Lys Ile Ile Leu Gln Gln Ile Pro Phe Thr Leu Thr Ala Leu	
290 295 300	
gtg ttg atg acg tcg gct ttt tgc tgg tta cta cat cgc tca ctg gcc	960
Val Leu Met Thr Ser Ala Phe Cys Trp Leu Leu His Arg Ser Leu Ala	
305 310 315 320	
aaa ccg tta tgg cgt ttt gtc gat gtc att aat aaa acc gca act gca	1008
Lys Pro Leu Trp Arg Phe Val Asp Val Ile Asn Lys Thr Ala Thr Ala	
325 330 335	
ccg ctg agc aca cgt tta cca gca caa cga ctg gat gaa tta gat agt	1056
Pro Leu Ser Thr Arg Leu Pro Ala Gln Arg Leu Asp Glu Leu Asp Ser	
340 345 350	
att gcc ggt gct ttt aac caa ctg ctt gat act cta caa gtc caa tac	1104
Ile Ala Gly Ala Phe Asn Gln Leu Leu Asp Thr Leu Gln Val Gln Tyr	
355 360 365	
gac aat ctg gaa aac aaa gtc gca gag cgc acc cag gcg cta aat gaa	1152
Asp Asn Leu Glu Asn Lys Val Ala Glu Arg Thr Gln Ala Leu Asn Glu	
370 375 380	
gca aaa aaa cgc gct gag cga gct aac aaa cgt aaa agc att cat ctt	1200
Ala Lys Lys Arg Ala Glu Arg Ala Asn Lys Arg Lys Ser Ile His Leu	
385 390 395 400	
acg gta ata agt cat gag tta cgt act ccg atg aat ggc gta ctc ggt	1248
Thr Val Ile Ser His Glu Leu Arg Thr Pro Met Asn Gly Val Leu Gly	
405 410 415	
gca att gaa tta tta caa acc acc cct tta aac ata gag caa caa gga	1296
Ala Ile Glu Leu Leu Gln Thr Thr Pro Leu Asn Ile Glu Gln Gln Gly	
420 425 430	

tta gct gat acc gcc aga aat tgt aca ctg tct ttg tta gct att att	1344
Leu Ala Asp Thr Ala Arg Asn Cys Thr Leu Ser Leu Leu Ala Ile Ile	
435 440 445	
aat aat ctg ctg gat ttt tca cgc atc gag tct ggt cat ttc aca tta	1392
Asn Asn Leu Leu Asp Phe Ser Arg Ile Glu Ser Gly His Phe Thr Leu	
450 455 460	
cat atg gaa gaa aca gcg tta ctg ccg tta ctg gac cag gca atg caa	1440
His Met Glu Glu Thr Ala Leu Leu Pro Leu Leu Asp Gln Ala Met Gln	
465 470 475 480	
acc atc cag ggg cca gcg caa agc aaa aaa ctg tca tta cgt act ttt	1488
Thr Ile Gln Gly Pro Ala Gln Ser Lys Lys Leu Ser Leu Arg Thr Phe	
485 490 495	
gtc ggt caa cat gtc cct ctc tat ttt cat acc gac agt atc cgt tta	1536
Val Gly Gln His Val Pro Leu Tyr Phe His Thr Asp Ser Ile Arg Leu	
500 505 510	
cgg caa att ttg gtt aat tta ctc ggg aac gcg gta aaa ttt acc gaa	1584
Arg Gln Ile Leu Val Asn Leu Leu Gly Asn Ala Val Lys Phe Thr Glu	
515 520 525	
acc gga ggg ata cgt ctg acg gtc aag cgt cat gag gaa caa tta ata	1632
Thr Gly Gly Ile Arg Leu Thr Val Lys Arg His Glu Glu Gln Leu Ile	
530 535 540	
ttt ctg gtt agc gat agc ggt aaa ggg att gaa ata cag cag cag tct	1680
Phe Leu Val Ser Asp Ser Gly Lys Gly Ile Glu Ile Gln Gln Gln Ser	
545 550 555 560	
caa atc ttt act gct ttt tat caa gca gac aca aat tcg caa ggt aca	1728
Gln Ile Phe Thr Ala Phe Tyr Gln Ala Asp Thr Asn Ser Gln Gly Thr	
565 570 575	
gga att gga ctg act att gcg tca agc ctg gct aaa atg atg ggc ggt	1776
Gly Ile Gly Leu Thr Ile Ala Ser Ser Leu Ala Lys Met Met Gly Gly	
580 585 590	
aat ctg aca cta aaa agt gtc ccc ggg gtt gga acc tgt gtc tcg cta	1824
Asn Leu Thr Leu Lys Ser Val Pro Gly Val Gly Thr Cys Val Ser Leu	
595 600 605	
gta tta ccc tta caa gaa tac cag ccg cct caa cca att aaa ggg acg	1872
Val Leu Pro Leu Gln Glu Tyr Gln Pro Pro Gln Pro Ile Lys Gly Thr	
610 615 620	
ctg tca gcg ccg ttc tgc ctg cat cgg caa ctg gct tgc tgg gga ata	1920
Leu Ser Ala Pro Phe Cys Leu His Arg Gln Leu Ala Cys Trp Gly Ile	
625 630 635 640	
cgc ggt gaa cca ccc cac cag caa aat gcg ctt ctc aac gca gag ctt	1968
Arg Gly Glu Pro Pro His Gln Gln Asn Ala Leu Leu Asn Ala Glu Leu	
645 650 655	
ttg tat ttc tcc gga aaa ctc tac gac ctg gcg caa cag tta ata ttg	2016

Leu	Tyr	Phe	Ser	Gly	Lys	Leu	Tyr	Asp	Leu	Ala	Gln	Gln	Leu	Ile	Leu	
			660					665					670			
tgt	aca	cca	aat	atg	cca	gta	ata	aat	aat	ttg	tta	cca	ccc	tggt	cag	2064
Cys	Thr	Pro	Asn	Met	Pro	Val	Ile	Asn	Asn	Leu	Leu	Pro	Pro	Trp	Gln	
		675					680					685				
ttg	cag	att	ctt	ttg	gtt	gat	gat	gcc	gat	att	aat	cgg	gat	atc	atc	2112
Leu	Gln	Ile	Leu	Leu	Val	Asp	Asp	Ala	Asp	Ile	Asn	Arg	Asp	Ile	Ile	
	690					695					700					
ggc	aaa	atg	ctt	gtc	agc	ctg	ggc	caa	cac	gtc	act	att	gcc	gcc	agt	2160
Gly	Lys	Met	Leu	Val	Ser	Leu	Gly	Gln	His	Val	Thr	Ile	Ala	Ala	Ser	
705					710					715					720	
agt	aac	gag	gct	ctg	act	tta	tca	caa	cag	cag	cga	ttc	gat	tta	gta	2208
Ser	Asn	Glu	Ala	Leu	Thr	Leu	Ser	Gln	Gln	Gln	Arg	Phe	Asp	Leu	Val	
				725					730					735		
ctg	att	gac	att	aga	atg	cca	gaa	ata	gat	ggg	att	gaa	tgt	gta	cga	2256
Leu	Ile	Asp	Ile	Arg	Met	Pro	Glu	Ile	Asp	Gly	Ile	Glu	Cys	Val	Arg	
			740					745					750			
tta	tggt	cat	gat	gag	ccg	aat	aat	tta	gat	cct	gac	tgc	atg	ttt	gtg	2304
Leu	Trp	His	Asp	Glu	Pro	Asn	Asn	Leu	Asp	Pro	Asp	Cys	Met	Phe	Val	
		755					760					765				
gca	cta	tcc	gct	agc	gta	gcg	aca	gaa	gat	att	cat	cgt	tgt	aaa	aaa	2352
Ala	Leu	Ser	Ala	Ser	Val	Ala	Thr	Glu	Asp	Ile	His	Arg	Cys	Lys	Lys	
	770					775					780					
aat	ggg	att	cat	cat	tac	att	aca	aaa	cca	gtg	aca	ttg	gct	acc	tta	2400
Asn	Gly	Ile	His	His	Tyr	Ile	Thr	Lys	Pro	Val	Thr	Leu	Ala	Thr	Leu	
785					790					795					800	
gct	cgc	tac	atc	agt	att	gcc	gca	gaa	tac	caa	ctt	tta	cga	aat	ata	2448
Ala	Arg	Tyr	Ile	Ser	Ile	Ala	Ala	Glu	Tyr	Gln	Leu	Leu	Arg	Asn	Ile	
				805					810					815		
gag	cta	cag	gag	cag	gat	ccg	agt	cgc	tgc	tca	gcg	cta	ctg	gcg	aca	2496
Glu	Leu	Gln	Glu	Gln	Asp	Pro	Ser	Arg	Cys	Ser	Ala	Leu	Leu	Ala	Thr	
			820					825					830			
gat	gat	atg	gtc	att	aat	agc	aag	att	ttc	caa	tca	ctg	gac	ctc	ttg	2544
Asp	Asp	Met	Val	Ile	Asn	Ser	Lys	Ile	Phe	Gln	Ser	Leu	Asp	Leu	Leu	
		835					840					845				
ctg	gct	gat	att	gaa	aat	gcc	gta	tcg	gct	gga	gaa	aaa	atc	gat	cag	2592
Leu	Ala	Asp	Ile	Glu	Asn	Ala	Val	Ser	Ala	Gly	Glu	Lys	Ile	Asp	Gln	
	850					855					860					
tta	att	cac	aca	tta	aaa	ggc	tgt	tta	ggg	caa	ata	ggg	cag	act	gaa	2640
Leu	Ile	His	Thr	Leu	Lys	Gly	Cys	Leu	Gly	Gln	Ile	Gly	Gln	Thr	Glu	
865					870					875					880	
ttg	gta	tgc	tat	gtc	ata	gac	att	gag	aat	cgc	gta	aaa	atg	ggg	aaa	2688
Leu	Val	Cys	Tyr	Val	Ile	Asp	Ile	Glu	Asn	Arg	Val	Lys	Met	Gly	Lys	

885								890				895				
atc	atc	gcg	ctg	gag	gaa	cta	acc	gac	tta	cgc	cag	aaa	ata	cgt	atg	2736
Ile	Ile	Ala	Leu	Glu	Glu	Leu	Thr	Asp	Leu	Arg	Gln	Lys	Ile	Arg	Met	
900								905				910				

atc	ttc	aaa	aac	tac	acc	att	act	taa	2763
Ile	Phe	Lys	Asn	Tyr	Thr	Ile	Thr		
915				920					

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 <213> Salmonella

<400> 35															
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Arg	Leu	Thr	Phe	Leu	Phe	Leu	Leu	Thr	Thr	Ile	Ile	Ile	Trp	Leu	Leu
			20					25					30		
Ser	Val	Leu	Thr	Ala	Ala	Tyr	Ile	Ser	Met	Val	Gln	Lys	Arg	Gln	His
		35					40					45			
Ile	Ile	Glu	Asp	Leu	Ser	Val	Leu	Ser	Glu	Met	Asn	Ile	Val	Leu	Ser
	50					55					60				
Asn	Gln	Arg	Phe	Glu	Glu	Ala	Glu	Arg	Asp	Ala	Lys	Asn	Leu	Met	Tyr
65					70					75					80
Gln	Cys	Ser	Leu	Ala	Thr	Glu	Ile	His	His	Asn	Asp	Ile	Phe	Pro	Glu
				85					90					95	
Val	Ser	Arg	His	Leu	Ser	Val	Gly	Pro	Ser	Asn	Cys	Thr	Pro	Thr	Leu
			100					105					110		
Asn	Gly	Glu	Lys	His	Arg	Leu	Phe	Leu	Gln	Ser	Ser	Asp	Ile	Asp	Glu
		115					120					125			
Asn	Ser	Phe	Arg	Arg	Asp	Ser	Phe	Ile	Leu	Asn	His	Lys	Asn	Glu	Ile
	130					135					140				
Ser	Leu	Leu	Ser	Thr	Asp	Asn	Pro	Ser	Asp	Tyr	Ser	Thr	Leu	Gln	Pro
145					150					155					160
Leu	Thr	Arg	Lys	Ser	Phe	Pro	Leu	Tyr	Pro	Thr	His	Ala	Gly	Phe	Tyr
			165						170					175	
Trp	Ser	Glu	Pro	Glu	Tyr	Ile	Asn	Gly	Lys	Gly	Trp	His	Ala	Ser	Val
		180						185					190		
Ala	Val	Ala	Asp	Gln	Gln	Gly	Val	Phe	Phe	Glu	Val	Thr	Val	Lys	Leu
		195					200					205			
Pro	Asp	Leu	Ile	Thr	Lys	Ser	His	Leu	Pro	Leu	Asp	Asp	Ser	Ile	Arg

210					215					220					
Val 225	Trp	Leu	Asp	Gln	Asn 230	Asn	His	Leu	Leu	Pro 235	Phe	Ser	Tyr	Ile	Pro 240
Gln	Lys	Ile	Arg	Thr 245	Gln	Leu	Glu	Asn	Val 250	Thr	Leu	His	Asp	Gly 255	Trp
Gln	Gln	Ile	Pro 260	Gly	Phe	Leu	Ile	Leu 265	Arg	Thr	Thr	Leu	His 270	Gly	Pro
Gly	Trp	Ser 275	Leu	Val	Thr	Leu	Tyr 280	Pro	Tyr	Gly	Asn	Leu 285	His	Asn	Arg
Ile	Leu 290	Lys	Ile	Ile	Leu	Gln 295	Gln	Ile	Pro	Phe	Thr 300	Leu	Thr	Ala	Leu
Val 305	Leu	Met	Thr	Ser	Ala 310	Phe	Cys	Trp	Leu	Leu 315	His	Arg	Ser	Leu	Ala 320
Lys	Pro	Leu	Trp	Arg 325	Phe	Val	Asp	Val	Ile 330	Asn	Lys	Thr	Ala	Thr 335	Ala
Pro	Leu	Ser	Thr 340	Arg	Leu	Pro	Ala	Gln 345	Arg	Leu	Asp	Glu	Leu 350	Asp	Ser
Ile	Ala	Gly 355	Ala	Phe	Asn	Gln	Leu 360	Leu	Asp	Thr	Leu	Gln 365	Val	Gln	Tyr
Asp	Asn 370	Leu	Glu	Asn	Lys	Val 375	Ala	Glu	Arg	Thr	Gln 380	Ala	Leu	Asn	Glu
Ala 385	Lys	Lys	Arg	Ala	Glu 390	Arg	Ala	Asn	Lys	Arg 395	Lys	Ser	Ile	His	Leu 400
Thr	Val	Ile	Ser	His 405	Glu	Leu	Arg	Thr	Pro 410	Met	Asn	Gly	Val	Leu 415	Gly
Ala	Ile	Glu	Leu 420	Leu	Gln	Thr	Thr	Pro 425	Leu	Asn	Ile	Glu	Gln 430	Gln	Gly
Leu	Ala	Asp 435	Thr	Ala	Arg	Asn	Cys 440	Thr	Leu	Ser	Leu	Leu 445	Ala	Ile	Ile
Asn	Asn 450	Leu	Leu	Asp	Phe	Ser 455	Arg	Ile	Glu	Ser	Gly 460	His	Phe	Thr	Leu
His 465	Met	Glu	Glu	Thr	Ala 470	Leu	Leu	Pro	Leu	Leu 475	Asp	Gln	Ala	Met	Gln 480
Thr	Ile	Gln	Gly	Pro 485	Ala	Gln	Ser	Lys	Lys 490	Leu	Ser	Leu	Arg	Thr 495	Phe
Val	Gly	Gln	His 500	Val	Pro	Leu	Tyr	Phe 505	His	Thr	Asp	Ser	Ile 510	Arg	Leu
Arg	Gln	Ile	Leu	Val	Asn	Leu	Leu	Gly	Asn	Ala	Val	Lys	Phe	Thr	Glu

515					520					525					
Thr	Gly	Gly	Ile	Arg	Leu	Thr	Val	Lys	Arg	His	Glu	Glu	Gln	Leu	Ile
530					535					540					
Phe	Leu	Val	Ser	Asp	Ser	Gly	Lys	Gly	Ile	Glu	Ile	Gln	Gln	Gln	Ser
545					550					555					560
Gln	Ile	Phe	Thr	Ala	Phe	Tyr	Gln	Ala	Asp	Thr	Asn	Ser	Gln	Gly	Thr
				565					570					575	
Gly	Ile	Gly	Leu	Thr	Ile	Ala	Ser	Ser	Leu	Ala	Lys	Met	Met	Gly	Gly
			580					585					590		
Asn	Leu	Thr	Leu	Lys	Ser	Val	Pro	Gly	Val	Gly	Thr	Cys	Val	Ser	Leu
		595					600					605			
Val	Leu	Pro	Leu	Gln	Glu	Tyr	Gln	Pro	Pro	Gln	Pro	Ile	Lys	Gly	Thr
	610					615					620				
Leu	Ser	Ala	Pro	Phe	Cys	Leu	His	Arg	Gln	Leu	Ala	Cys	Trp	Gly	Ile
625					630					635					640
Arg	Gly	Glu	Pro	Pro	His	Gln	Gln	Asn	Ala	Leu	Leu	Asn	Ala	Glu	Leu
				645					650					655	
Leu	Tyr	Phe	Ser	Gly	Lys	Leu	Tyr	Asp	Leu	Ala	Gln	Gln	Leu	Ile	Leu
			660					665					670		
Cys	Thr	Pro	Asn	Met	Pro	Val	Ile	Asn	Asn	Leu	Leu	Pro	Pro	Trp	Gln
		675					680					685			
Leu	Gln	Ile	Leu	Leu	Val	Asp	Asp	Ala	Asp	Ile	Asn	Arg	Asp	Ile	Ile
	690					695					700				
Gly	Lys	Met	Leu	Val	Ser	Leu	Gly	Gln	His	Val	Thr	Ile	Ala	Ala	Ser
705					710					715					720
Ser	Asn	Glu	Ala	Leu	Thr	Leu	Ser	Gln	Gln	Gln	Arg	Phe	Asp	Leu	Val
				725					730					735	
Leu	Ile	Asp	Ile	Arg	Met	Pro	Glu	Ile	Asp	Gly	Ile	Glu	Cys	Val	Arg
			740					745					750		
Leu	Trp	His	Asp	Glu	Pro	Asn	Asn	Leu	Asp	Pro	Asp	Cys	Met	Phe	Val
		755					760					765			
Ala	Leu	Ser	Ala	Ser	Val	Ala	Thr	Glu	Asp	Ile	His	Arg	Cys	Lys	Lys
	770					775					780				
Asn	Gly	Ile	His	His	Tyr	Ile	Thr	Lys	Pro	Val	Thr	Leu	Ala	Thr	Leu
785					790					795					800
Ala	Arg	Tyr	Ile	Ser	Ile	Ala	Ala	Glu	Tyr	Gln	Leu	Leu	Arg	Asn	Ile
				805					810					815	
Glu	Leu	Gln	Glu	Gln	Asp	Pro	Ser	Arg	Cys	Ser	Ala	Leu	Leu	Ala	Thr



820					825					830					
Asp	Asp	Met	Val	Ile	Asn	Ser	Lys	Ile	Phe	Gln	Ser	Leu	Asp	Leu	Leu
835					840					845					
Leu	Ala	Asp	Ile	Glu	Asn	Ala	Val	Ser	Ala	Gly	Glu	Lys	Ile	Asp	Gln
850					855					860					
Leu	Ile	His	Thr	Leu	Lys	Gly	Cys	Leu	Gly	Gln	Ile	Gly	Gln	Thr	Glu
865					870					875					
Leu	Val	Cys	Tyr	Val	Ile	Asp	Ile	Glu	Asn	Arg	Val	Lys	Met	Gly	Lys
885					890					895					
Ile	Ile	Ala	Leu	Glu	Glu	Leu	Thr	Asp	Leu	Arg	Gln	Lys	Ile	Arg	Met
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Ile	Phe	Lys	Asn	Tyr	Thr	Ile	Thr								
915					920										

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 <212> DNA  
 <213> Salmonella

<220>  
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Met	Lys	Glu	Tyr	Lys	Ile	Leu	Leu	Val	Asp	Asp	His	Glu	Ile	Ile	Ile	
1				5				10					15			
aac ggc att atg aat gcc tta tta ccc tgg cct cat ttt aaa att gta															96	
Asn	Gly	Ile	Met	Asn	Ala	Leu	Leu	Pro	Trp	Pro	His	Phe	Lys	Ile	Val	
			20					25					30			
gag cat gtt aaa aat ggt ctt gag gtt tat aat gcc tgt tgt gca tac															144	
Glu	His	Val	Lys	Asn	Gly	Leu	Glu	Val	Tyr	Asn	Ala	Cys	Cys	Ala	Tyr	
		35				40						45				
gag cct gac ata ctt atc ctt gat ctt agt cta cct ggc atc aat ggc															192	
Glu	Pro	Asp	Ile	Leu	Ile	Leu	Asp	Leu	Ser	Leu	Pro	Gly	Ile	Asn	Gly	
	50					55					60					
ctg gat atc att cct caa tta cat cag cgt tgg cca gca atg aat att															240	
Leu	Asp	Ile	Ile	Pro	Gln	Leu	His	Gln	Arg	Trp	Pro	Ala	Met	Asn	Ile	
65					70					75					80	
ctg gtt tac aca gca tac caa caa gag tat atg acc att aaa act tta															288	
Leu	Val	Tyr	Thr	Ala	Tyr	Gln	Gln	Glu	Tyr	Met	Thr	Ile	Lys	Thr	Leu	
			85					90						95		
gcc gca ggt gct aat ggc tat gtt tta aaa agc agt agt cag caa gtt															336	

Ala	Ala	Gly	Ala	Asn	Gly	Tyr	Val	Leu	Lys	Ser	Ser	Ser	Gln	Gln	Val		
			100					105					110				
ctg	tta	gcg	gca	ttg	caa	aca	gta	gca	gta	aac	aag	cgt	tac	att	gac	384	
Leu	Leu	Ala	Ala	Leu	Gln	Thr	Val	Ala	Val	Asn	Lys	Arg	Tyr	Ile	Asp		
			115				120					125					
cca	acg	ttg	aat	cgg	gaa	gct	atc	ctg	gct	gaa	tta	aac	gct	gac	acg	432	
Pro	Thr	Leu	Asn	Arg	Glu	Ala	Ile	Leu	Ala	Glu	Leu	Asn	Ala	Asp	Thr		
			130				135					140					
acc	aat	cat	caa	ctg	ctt	act	ttg	cgc	gag	cgt	cag	gtt	ctt	aaa	ctt	480	
Thr	Asn	His	Gln	Leu	Leu	Thr	Leu	Arg	Glu	Arg	Gln	Val	Leu	Lys	Leu		
					150					155					160		
att	gac	gag	ggg	tat	acc	aat	cat	ggg	atc	agc	gaa	aag	cta	cat	atc	528	
Ile	Asp	Glu	Gly	Tyr	Thr	Asn	His	Gly	Ile	Ser	Glu	Lys	Leu	His	Ile		
				165					170						175		
agt	ata	aaa	acc	gtc	gaa	aca	cac	cgg	atg	aat	atg	atg	aga	aag	cta	576	
Ser	Ile	Lys	Thr	Val	Glu	Thr	His	Arg	Met	Asn	Met	Met	Arg	Lys	Leu		
			180					185					190				
cag	gtt	cat	aaa	gtg	aca	gag	tta	ctt	aac	tgt	gcc	cga	aga	atg	agg	624	
Gln	Val	His	Lys	Val	Thr	Glu	Leu	Leu	Asn	Cys	Ala	Arg	Arg	Met	Arg		
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tta	ata	gag	tat	taa												639	
Leu	Ile	Glu	Tyr														
				210													
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<400> 37																	
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Asn	Gly	Ile	Met	Asn	Ala	Leu	Leu	Pro	Trp	Pro	His	Phe	Lys	Ile	Val		
			20					25					30				
Glu	His	Val	Lys	Asn	Gly	Leu	Glu	Val	Tyr	Asn	Ala	Cys	Cys	Ala	Tyr		
		35					40					45					
Glu	Pro	Asp	Ile	Leu	Ile	Leu	Asp	Leu	Ser	Leu	Pro	Gly	Ile	Asn	Gly		
		50				55					60						
Leu	Asp	Ile	Ile	Pro	Gln	Leu	His	Gln	Arg	Trp	Pro	Ala	Met	Asn	Ile		
		65			70					75					80		
Leu	Val	Tyr	Thr	Ala	Tyr	Gln	Gln	Glu	Tyr	Met	Thr	Ile	Lys	Thr	Leu		
				85					90						95		
Ala	Ala	Gly	Ala	Asn	Gly	Tyr	Val	Leu	Lys	Ser	Ser	Ser	Gln	Gln	Val		

100	105	110
Leu Leu Ala Ala Leu Gln Thr Val Ala Val Asn Lys Arg Tyr Ile Asp		
115	120	125
Pro Thr Leu Asn Arg Glu Ala Ile Leu Ala Glu Leu Asn Ala Asp Thr		
130	135	140
Thr Asn His Gln Leu Leu Thr Leu Arg Glu Arg Gln Val Leu Lys Leu		
145	150	155
Ile Asp Glu Gly Tyr Thr Asn His Gly Ile Ser Glu Lys Leu His Ile		
165	170	175
Ser Ile Lys Thr Val Glu Thr His Arg Met Asn Met Met Arg Lys Leu		
180	185	190
Gln Val His Lys Val Thr Glu Leu Leu Asn Cys Ala Arg Arg Met Arg		
195	200	205
Leu Ile Glu Tyr		
210		

<210> 38  
 <211> 388  
 <212> DNA  
 <213> Salmonella

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 aaccagtcg atgactacaa ttacttttta ataagatggc gatgtaaaaa catcgtaaca 180  
 gtttatttaa taaataattt ttcaaattgt aagtttttat gtcaatgctg aaaatgtaat 240  
 tgtgaattta tcggaaaaatc cgaatgatag aatcgccctgt gacaaggat atgtagacag 300  
 catcctgata ttgtacaaga agagatagtc gaaataaatg tgaatcaggc tttttacgga 360  
 tgtggttggt agcgaaatttg atagaaac 388

<210> 39  
 <211> 262  
 <212> DNA  
 <213> Salmonella

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 atagcgcgca aaaaccgcag cgtacacgta gtacgtgagg tttgactcgc tacgctcgcc 120  
 cttcgggccg ccgctagcgg cgttcaaaac gctaacgcgt tttggcgagc actgcccagg 180  
 ttcaaaatgg caagtaaaat agcctaattg gataggctct tagttagcac gttaattatc 240  
 tatcgtgtat atggagggga at 262

<210> 40  
 <211> 192  
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<300>

<303> Mol. Microbiol.

<304> 28

<306> 1-4

<307> 1998

<400> 40

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Ser Thr Ser Met Ala Tyr Asp Leu Gly Ser Met Ser Lys Asp Asp Val  
20 25 30

Ile Asp Leu Phe Asn Lys Leu Gly Val Phe Gln Ala Ala Ile Leu Met  
35 40 45

Phe Ala Tyr Met Tyr Gln Ala Gln Ser Asp Leu Ser Ile Ala Lys Phe  
50 55 60

Ala Asp Met Asn Glu Ala Ser Lys Glu Ser Thr Thr Ala Gln Lys Met  
65 70 75 80

Ala Asn Leu Val Asp Ala Lys Ile Ala Asp Val Gln Ser Ser Ser Asp  
85 90 95

Lys Asn Ala Lys Ala Gln Leu Pro Asp Glu Val Ile Ser Tyr Ile Asn  
100 105 110

Asp Pro Arg Asn Asp Ile Thr Ile Ser Gly Ile Asp Asn Ile Asn Ala  
115 120 125

Gln Leu Gly Ala Gly Asp Leu Gln Thr Val Lys Ala Ala Ile Ser Ala  
130 135 140

Lys Ala Asn Asn Leu Thr Thr Thr Val Asn Asn Ser Gln Leu Glu Ile  
145 150 155 160

Gln Gln Met Ser Asn Thr Leu Asn Leu Leu Thr Ser Ala Arg Ser Asp  
165 170 175

Met Gln Ser Leu Gln Tyr Arg Thr Ile Ser Gly Ile Ser Leu Gly Lys  
180 185 190

<210> 41

<211> 380

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<304> 28

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<307> 1998

<400> 41

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			20					25					30			
Leu	Asp	Leu	Gln	Leu	Val	Lys	Ser	Thr	Ala	Pro	Ser	Ala	Ser	Trp	Thr	
		35					40					45				
Glu	Ser	Thr	Ala	Leu	Ala	Thr	Pro	Pro	Ala	Gly	His	Ser	Leu	Val	Thr	
	50					55					60					
Pro	Ser	Ala	Ala	Glu	Asp	Val	Leu	Ser	Lys	Leu	Phe	Gly	Gly	Ile	Ser	
65					70					75					80	
Gly	Glu	Val	Thr	Ser	Arg	Thr	Glu	Gly	Thr	Glu	Pro	Gln	Arg	Ser	Thr	
				85					90					95		
Gln	Asn	Ala	Ser	Ser	Gly	Tyr	Pro	Tyr	Leu	Ser	Gln	Val	Asn	Asn	Val	
			100					105					110			
Asp	Pro	Gln	Ala	Met	Met	Met	Met	Ala	Thr	Leu	Leu	Ser	Leu	Asp	Ala	
		115					120					125				
Ser	Ala	Gln	Arg	Val	Ala	Ser	Met	Lys	Asn	Ser	Asn	Glu	Ile	Tyr	Ala	
	130					135					140					
Asp	Gly	Gln	Asn	Lys	Ala	Leu	Asp	Asn	Lys	Thr	Leu	Glu	Phe	Lys	Lys	
145				150					155						160	
Gln	Leu	Glu	Glu	Gln	Gln	Lys	Ala	Glu	Glu	Lys	Ala	Gln	Lys	Ser	Lys	
			165					170						175		
Ile	Val	Gly	Gln	Val	Phe	Gly	Trp	Leu	Gly	Val	Ala	Ala	Thr	Ala	Ile	
		180					185						190			
Ala	Ala	Ile	Phe	Asn	Pro	Ala	Leu	Trp	Ala	Val	Val	Ala	Ile	Ser	Ala	
		195				200						205				
Thr	Ala	Met	Ala	Leu	Gln	Thr	Ala	Val	Asp	Val	Met	Gly	Asp	Asp	Ala	
	210				215						220					
Pro	Gln	Ala	Leu	Lys	Thr	Ala	Ala	Gln	Ala	Phe	Gly	Gly	Leu	Ser	Leu	
225				230					235						240	
Ala	Ala	Gly	Ile	Leu	Thr	Ala	Gly	Ile	Gly	Gly	Val	Ser	Ser	Leu	Ile	
			245					250						255		
Ser	Lys	Val	Gly	Asp	Val	Ala	Asn	Lys	Val	Gly	Ser	Asn	Ile	Val	Lys	
		260					265					270				
Val	Val	Thr	Thr	Leu	Ala	Asp	Thr	Phe	Val	Asp	Asn	Val	Ala	Ser	Lys	
		275				280					285					

Ile Ser Ala Val Ala Asn Gly Leu Thr Thr Ser Ser Arg Ser Ile Gly  
 290 295 300  
 Thr Thr Val Leu Asn Asn Asp Ala Ala Tyr Tyr Asn Val Leu Ser Gln  
 305 310 315 320  
 Val Ser Ala Phe Ala Val Glu Asn Leu Thr Arg Gln Ser Glu Tyr Leu  
 325 330 335  
 Ser Gln Ser Ala Lys Ala Glu Leu Glu Lys Ala Thr Leu Glu Leu Gln  
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 Ala Arg Val Asn Ile Arg Ile Val Ser Gly Arg Val  
 370 375 380

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 <213> *Yersinia enterocolitica*

<300>  
 <301> Hakansson, S.  
 Schesser, K.  
 Persson, C.  
 Galyov, E. E.  
 Rosqvist, R.  
 Homble, F.  
 Wolf Watz, H.  
 <303> EMBO J.  
 <304> 15  
 <306> 5812-5823  
 <307> 1996

<400> 42  
 Met Ser Ala Leu Ile Thr His Asp Arg Ser Thr Pro Val Thr Gly Ser  
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 Gly Val Gln Leu Pro Ala Pro Leu Ala Val Val Ala Ser Gln Val Thr  
 50 55 60  
 Glu Gly Gln Gln Gln Glu Ile Thr Lys Leu Leu Glu Ser Val Thr Arg  
 65 70 75 80  
 Gly Thr Ala Gly Ser Gln Leu Ile Ser Asn Tyr Val Ser Val Leu Thr  
 85 90 95

Asn	Phe	Thr	Leu	Ala	Ser	Pro	Asp	Thr	Phe	Glu	Ile	Glu	Leu	Gly	Lys		
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Leu	Val	Ser	Asn	Leu	Glu	Glu	Val	Arg	Lys	Asp	Ile	Lys	Ile	Ala	Asp		
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Glu	Lys	Ile	Lys	Glu	Thr	Glu	Glu	Asn	Ala	Lys	Gln	Val	Lys	Lys	Ser		
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Val	Ile	Gly	Ala	Ile	Met	Val	Ala	Ser	Gly	Val	Gly	Ala	Val	Ala	Gly		
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Lys	Gln	Ala	Ala	Glu	Asp	Gly	Leu	Ile	Ser	Gln	Glu	Ala	Met	Gln	Val		
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225					230					235					240		
Thr	Val	Met	Thr	Phe	Gly	Gly	Ser	Ala	Leu	Lys	Cys	Leu	Ala	Asp	Ile		
				245					250					255			
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			260					265					270				
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Val	Gly	Ser	Ala	Val	Thr	Lys	Leu	Gly	Gly	Ser	Phe	Gly	Ser	Leu	Thr		
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Gly	Val	Gly	Ser	Gly	Ile	Thr	Gln	Thr	Ile	Asn	Asn	Lys	Lys	Gln	Ala		
				325					330					335			
Asp	Leu	Gln	His	Asn	Asn	Ala	Asp	Leu	Ala	Leu	Asn	Lys	Ala	Asp	Met		
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<211> 390  
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<213> *Pseudomonas aeruginosa*

<300>  
<301> Hauser, A. R.  
Fleiszig, S.  
Kang, P. J.  
Mostov, K.  
Engel, J. N.  
<303> Infect. Immun.  
<304> 66  
<306> 1413-1420  
<307> 1998

<400> 43  
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35 40 45  
Ser Gly Thr Gly Val Ala Leu Thr Pro Pro Ser Ala Ala Ser Gln Gln  
50 55 60  
Arg Leu Glu Val Ala Asn Arg Ala Glu Ile Ala Ser Leu Val Gln Ala  
65 70 75 80  
Val Gly Glu Asp Ala Gly Leu Ala Arg Gln Val Val Leu Ala Gly Ala  
85 90 95  
Ser Thr Leu Leu Ser Ala Gly Leu Met Ser Pro Gln Ala Phe Glu Ile  
100 105 110  
Glu Leu Ala Lys Ile Thr Gly Glu Val Glu Asn Gln Gln Lys Lys Leu  
115 120 125  
Lys Leu Thr Glu Ile Glu Gln Ala Arg Lys Gln Asn Leu Gln Lys Met  
130 135 140  
Glu Asp Asn Gln Gln Lys Ile Arg Glu Ser Glu Glu Ala Ala Lys Glu  
145 150 155 160  
Ala Gln Lys Ser Gly Leu Ala Ala Lys Ile Phe Gly Trp Ile Ser Ala  
165 170 175  
Ile Ala Ser Ile Ile Val Gly Ala Ile Met Val Ala Thr Gly Val Gly



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210					215					220						
Val	Met	Glu	Lys	Leu	Gly	Pro	Ala	Leu	Met	Gly	Ile	Glu	Ile	Ala	Val	
225					230					235					240	
Ala	Leu	Leu	Ala	Ala	Val	Val	Ser	Phe	Gly	Gly	Ser	Ala	Val	Gly	Gly	
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Leu	Ala	Lys	Leu	Gly	Ala	Lys	Ile	Gly	Gly	Lys	Ala	Ala	Glu	Met	Thr	
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Ala	Ser	Leu	Ala	Ser	Lys	Val	Ala	Asn	Leu	Gly	Gly	Lys	Phe	Gly	Ser	
275					280					285						
Leu	Ala	Gly	Gln	Ser	Leu	Ser	His	Ser	Leu	Lys	Leu	Gly	Val	Gln	Val	
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Ser	Gly	Phe	Gln	Ala	Lys	Ala	Ala	Asn	Arg	Gln	Ala	Asp	Val	Gln	Glu	
325					330					335						
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Ile	Phe	Ala	Met	Leu	Gln	Ala	Lys	Gly	Glu	Thr	Leu	His	Asn	Leu	Ser	
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gctaagctta gagatgtatt agatacc 27

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27